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OM protein - protein search, using sw model

Run on: October 1, 2003, 18:52:57 ; Search time 82 Seconds
(without alignments)
29.035 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPRPPYLPFRPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	15	21	PR-39 derived angi
2	90	100.0	15	22	Amino acid sequenc
3	90	100.0	15	22	PR-39 derived pept
4	90	100.0	19	17	Leukocyte O2- prod
5	90	100.0	26	17	AAW01447
6	90	100.0	26	19	AAW75723
7	90	100.0	39	14	Proline/Arginine r
8	90	100.0	39	17	Antibacterial pept
9	90	100.0	39	17	Leukocyte O2- prod
					Synducin peptide (

10	90	100.0	39	17	AAW75722
11	90	100.0	39	19	AAW75722
12	90	100.0	39	21	AAW75722
13	90	100.0	39	22	AAW75722
14	90	100.0	39	22	AAW75722
15	90	100.0	42	23	AAW75722
16	90	100.0	44	22	AAW75722
17	83	92.2	14	17	AAW01450
18	83	92.2	14	19	AAW75725
19	75	83.3	23	17	AAW01451
20	66	73.3	18	16	AAW79211
21	66	73.3	20	19	AAW75730
22	66	73.3	23	16	AAW79209
23	66	73.3	35	16	AAW79212
24	66	73.3	59	19	AAW66400
25	66	73.3	59	21	AAW91699
26	66	73.3	59	24	AAW59576
27	66	73.3	60	23	ABW07713
28	66	73.3	62	22	ABW51197
29	64	71.1	11	21	ABW26886
30	64	71.1	11	22	ABW4652
31	64	71.1	11	22	ABW97278
32	64	71.1	11	24	ABG33050
33	63	70.0	91	22	AAW61229
34	61	67.8	336	17	AAW05520
35	60	66.7	953	23	AAW74761
36	60	66.7	953	23	AAW28708
37	59	65.6	38	24	ABW01253
38	59	65.6	38	24	ABW99763
39	59	65.6	39	21	AAW44779
40	59	65.6	59	17	AAW94448
41	56.5	62.8	74	22	ABW58034
42	56.5	62.8	74	22	ABW42619
43	56.5	62.8	74	22	ABW63510
44	56.5	62.8	74	22	AAW76344
45	56.5	62.8	74	22	AAW36433

ALIGNMENTS

RESULT 1
AAB26885
ID AAB26885 standard; peptide: 15 AA.
AC AAB26885;
XX
DT 01-FEB-2001 (first entry)
XX
DE PR-39 derived angiogenesis regulatory peptide 1.
XX
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW myocardial ischaemia; proteasome.
XX
OS Synthetic.
XX
FN WO200057895-A1.
XX
PD 05-OCT-2000.
XX
PF 16-MAR-2000; 2000WO-US07050.
XX
PR 26-MAR-1999; 99US-0276868.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2000-628319/60.
XX
PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
PT infarction, by administering a PR-39 oligopeptide that regulates
PT enzymatic activity of proteasomes -

Magainin-derived a
Proline/Arginine r
PR-39 peptide used
Amino acid sequenc
PR-39 peptide. Un
Antimicrobial pept
E. coli AMP gene p
Leukocyte O2- prod
Proline/Arginine r
Leukocyte O2- prod
Bactenecin peptide
Bactenecin peptide
Cationic peptide B
Cationic peptide B
Antimicrobial pept
E. coli AMP gene B
PR-39 derived angi
Amino acid sequenc
PR-39 derived pept
Pig arg/pro rich p
Propionibacterium
HCMV Toledo strain
Human protease PRT
Amino acid sequenc
Human gene 307-enc
Human secreted pro
Human secreted pro
Synducin peptide {
Human liver peptid
Peptide #10125 enc
Human brain expres
Human bone marrow
Peptide #10470 enc

XX PS Claim 12; Page 40; 51pp; English.

CC This invention relates to a method for the stimulation of angiogenesis in

CC situ within a targeted collection of viable cells. The method comprises

CC introducing, into the cytoplasm, at least a member of the PR-39

CC oligopeptide collective, which interacts with cytoplasmic proteasomes.

CC Part of the proteolytic activity of the proteasomes is selectively

CC altered so as to stimulate angiogenesis. The method is used to induce

CC angiogenesis in tissue that has suffered anoxia or infarction,

CC e.g. myocardial infarction or chronic myocardial ischaemia, and also to

CC study the mechanisms that control angiogenesis. The present sequence

CC represents a PR-39 derived peptide which interacts with the proteasome

CC and can be used in the method of the invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 21; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

RESULT 2

AA84691

ID AAB84691 standard; peptide; 15 AA.

AC AAB84691;

17-SEP-2001 (first entry)

Amino acid sequence of a PR-39 derived peptide (residues 1-15).

PR-39; IkappaBalpha degradation; NFkappaB transcription factor;

myocardial infarction; chronic myocardial ischemia; heart disease;

anoxia.

Unidentified.

WO200147540-A1.

05-JUL-2001.

27-DEC-2000; 2000WO-US35293.

29-DEC-1999; 99US-0474967.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Simons M, Gao Y;

WPI; 2001-441690/47.

Selective inhibition of IkappaBalpha degradation within targeted viable

cell collection, involves interacting PR-39 oligopeptide with

IkappaBalpha and proteasomes, and altering proteolytic activity of

proteasomes -

Claim 11; Page 58; 69pp; English.

The present sequence represents a PR-39 derived peptide. It is used

for selective inhibition of IkappaBalpha degradation within a targeted

cell collection in-situ. The method is useful for selectively inhibiting

IkappaBalpha protein degradation in situ, decreasing the activity of

NFkappaB transcription factor and selective control of NFkappaB-dependent

gene expression in situ. The PR-39 derived peptides are useful in the

treatment of myocardial infarction, chronic myocardial ischemia of

heart disease and anoxia.

Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

DB 1 RRRPRPPYLPRPP 15

RESULT 3

AA897277

ID AAB97277 standard; peptide; 15 AA.

AC AAB97277;

09-AUG-2001 (first entry)

PR-39 derived peptide PR-15.

PR-39; cathelin; inflammation; wound healing; myocardial infarction;

proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;

anoxia; chronic myocardial ischaemia; heart tissue.

Unidentified.

WO200130368-A1.

03-MAY-2001.

06-OCT-2000; 2000WO-US27552.

25-OCT-1999; 99US-0426011.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Simons M, Gao Y;

WPI; 2001-355179/37.

Stimulation of angiogenesis and inhibition of proteasome mediated

degradation in cells, by introduction of PR-39 oligopeptide or its

N-terminal fragments or their conjugates, for use in anoxia and

infarction conditions -

Claim 12; Page 42; 52pp; English.

Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39

is a member of the the cathelin family of proteins, mature PR-39 is 39

amino acids in length (see AAB97280), and has been shown to play a role

in several inflammatory events including wound healing and myocardial

infarction. The PR-39 derived family of oligopeptides cause selective

inhibition of proteasome mediated degeneration of peptides and

stimulation of angiogenesis after their intracellular introduction to a

target cell. PR-39 derived peptides are able to interact with at least

the alpha7 subunit of the proteasomes, and therefore alter the

proteolytic activity of proteasomes such that a selective increased

expression of specific proteins occurs. The invention includes methods

for the selective inhibition of proteasome mediated peptide degradation.

The method provides means for stimulating angiogenesis as required in

living tissues and organs which have suffered defects or have undergone

anoxia and/or infarction, myocardial infarction or chronic myocardial

ischaemia of heart tissue. Examples are the myocardium, skeletal or

smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,

gastrointestinal or nerve tissues, limbs, and extremities. A particular

example is after myocardial infarction or ischaemia.

Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15
 DB 1 RRRPRPPYLP RPP 15

RESULT 4

AAW01452
 ID AAW01452 standard; peptide; 19 AA.

AC AAW01452;

DT 18-JUN-1997 (first entry)

DE Leukocyte O2- production inhibitor peptide PR19.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04674.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte super:oxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39

XX Disclosure; Page 27; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting
 CC tissue damage at the wound site caused by excessive oxygen radicals
 CC produced by these leukocytes. They can also be used to develop products
 CC for treating inflammatory disease states.

XX Sequence 19 AA;

Query Match 100.0%; Score 90; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.0003;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15

DB 1 RRRPRPPYLP RPP 15

RESULT 5

AAW01447
 ID AAW01447 standard; peptide; 26 AA.

XX

AC

DT

18-JUN-1997 (first entry)

Leukocyte O2- production inhibitor peptide PR26.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 KW tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04674.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.

XX Inhibition of leukocyte super:oxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39

XX Claim 3; Page 26; 45pp; English.

XX AAW01447-W01454 represent fragments of the proline-arginine rich
 CC antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
 CC isolated from porcine small intestine, and has also been identified in
 CC human and porcine neutrophils. PR39 kills bacteria by interfering with
 CC DNA and/or protein synthesis. PR39 also induces syndecan expression on
 CC mesenchymal cells. Syndecans are important in wound repair, showing that
 CC PR39 can be used in wound repair, as well as in antibacterial agents.
 CC These sequences, and PR39, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting
 CC tissue damage at the wound site caused by excessive oxygen radicals
 CC produced by these leukocytes. They can also be used to develop products
 CC for treating inflammatory disease states.

XX Sequence 26 AA;

Query Match 100.0%; Score 90; DB 17; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15

DB 1 RRRPRPPYLP RPP 15

RESULT 6

AAW75723
 ID AAW75723 standard; peptide; 26 AA.

XX AAW75723;

XX 19-NOV-1998 (first entry)

XX Proline/Arginine rich peptide PR-26.

XX Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;

KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 XX coronary bypass; organ transplantation surgery.

OS Synthetic.

XX WO9835690-A1.

XX 20-AUG-1998.

XX 17-FEB-1998; 98WO-US03207.

XX 16-FEB-1998; 98US-0024975.

XX 18-FEB-1997; 97US-0802306.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Ross CR, Shi J;

XX WPI; 1998-495359/42.

XX Reduction of reperfusion injury in temporarily occluded blood
 XX vessels - by administration of a peptide which is rich in proline
 XX or arginine residues

XX Claim 3; Page 14-15; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 XX administration into a mammal's bloodstream reduce reperfusion injury
 XX (production of reactive oxygen species, neutrophil adherence to
 XX endothelium, and extravasation of neutrophils). These peptides have two
 XX requirements: they contain the consensus sequence PXXP, where P is a
 XX proline residue and X is any amino acid residue, which has been found to
 XX inhibit superoxide production, and secondly they have arginine residues
 XX adjacent to these motifs, required for effective inhibition. It was
 XX established by structural and function analysis that a peptide should
 XX ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 XX correlated with the increase of length of peptides. The effectiveness
 XX of these peptides was determined by investigating the production of the
 XX neutrophil superoxide anion, and also the inhibition of neutrophil
 XX chemotaxis. From this, it was found that all of the peptides inhibited
 XX NADPH oxidase to some extent. All of the peptides also inhibit
 XX neutrophil oxidase activity. PR-39 is believed, to be the most potent
 XX endogenous down regulator of NADPH oxidase yet discovered, and from the
 XX data produced, it can be suggested to be involved in eliminating or
 XX reducing the reperfusion injury induced adhesion and extraction of
 XX neutrophils. The peptides are also useful in connection with surgical
 XX procedures such as coronary bypass and organ transplantation surgery.

XX Sequence 26 AA;

Query Match 100.0%; Score 90; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRPP 15
 |||||
 Db 1 RRRPRPPYLP RPRPP 15

RESULT 7

AAAR30491

ID AAR30491 standard; peptide; 39 AA.

XX AC AAR30491;

XX 25-MAR-2003 (updated)

DT 12-MAY-1993 (first entry)

XX Antibacterial peptide.

XX Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
 XX veterinary medicine; prophylactic.

OS Sus scrofa domestica.

XX WO9222578-A1.

XX 23-DEC-1992.

XX 10-JUN-1992; 92WO-SB00394.

XX 14-JUN-1991; 91SE-0001838.

XX (BONA/) BOMAN H G.

XX (JOER/) JOERNVALL H.

XX (LEEJ/) LEE J.

XX (MUTT/) MUTT V.

XX Boman HG, Joernvall H, Lee J, Mutt V;

XX WPI; 1993-018080/02.

XX New anti-bacterial polypeptide - active against Gram negative

XX bacteria

XX Claim 1; Page 10; 15pp; English.

XX This peptide was isolated from the small intestine of a pig. The
 XX small intestine is an important endocrine organ and many it. This
 XX physiologically active peptides have been isolated from it. This
 XX peptide inhibits the growth of, and may kill, bacteria, pref. gram
 XX negative bacteria. This peptide or its functional derivatives may be
 XX used in human or veterinary medicine for therapeutic or prophylactic
 XX use.
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 39 AA;

Query Match 100.0%; Score 90; DB 14; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRPP 15
 |||||
 Db 1 RRRPRPPYLP RPRPP 15

RESULT 8

AAW01446

ID AAW01446 standard; peptide; 39 AA.

XX AC AAW01446;

XX 18-JUN-1997 (first entry)

XX Leukocyte O2- production inhibitor peptide PR39.

XX Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
 XX antimicrobial peptide; small intestine; human; neutrophil; bacteria;
 XX DNA synthesis; protein synthesis; inhibitor; syndecan expression;
 XX mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
 XX tissue damage; oxygen radical; inflammatory disease; therapy.

XX Synthetic.

XX WO9632129-A1.

XX 17-OCT-1996.

XX 10-APR-1996; 96WO-US04574.

XX 10-APR-1995; 95US-0419066.

XX (UNIV) UNIV KANSAS STATE RES FOUND.

XX Blecha F, Shi J;

XX WPI; 1996-476842/47.
 XX Inhibition of leukocyte superoxide anion prodn. and attraction of
 PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39
 XX
 XX Claim 2; Page 26; 45pp; English.
 XX
 XX This sequence represents the proline-arginine rich antimicrobial peptide
 CC PR39. The PR39 sequence was first isolated from porcine small intestine,
 CC and has also been identified in human and porcine neutrophils. PR39
 CC kills bacteria by interfering with DNA and/or protein synthesis. PR39
 CC also induces syndecan expression on mesenchymal cells. Syndecans are
 CC important in wound repair, showing that PR39 can be used in wound repair,
 CC as well as in antibacterial agents. This sequence, and the fragments of
 CC it shown in AA01447-W01454, can be used in the method of the invention.
 CC The method of the invention is for inhibiting leukocyte superoxide anion
 CC (O2-) production. The method comprises administering to a leukocyte a
 CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
 CC production. The peptides can be used as medicaments for fighting
 CC infection by attracting leukocytes to a wound site and restricting tissue
 CC damage at the wound site caused by excessive oxygen radicals produced by
 CC these leukocytes. They can also be used to develop products for treating
 CC inflammatory disease states.
 XX
 XX SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 17; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPFRPP 15
 |||||
 DB 1 RRRPPPYLPFRPP 15

RESULT 9
 AAR94446
 - ID AAR94446 standard; peptide; 39 AA.

XX AAR94446;
 XX
 XX 05-NOV-1996 (first entry)
 XX
 XX Syndecan peptide (PR-39) induces syndecan expression.
 XX
 XX Syndecan; induction; expression; syndecan-1; syndecan-4; surface;
 XX mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
 XX decubitus; ulcers; keloids; skin burns; ischemic tissues;
 XX hypercoagulation states; prevention; tumour metastasis; restenosis;
 XX inhibition; angiogenesis; proliferation; tumour metastasis; restenosis;
 XX
 XX Synthetic.

XX
 XX W09609322-A2.
 XX 28-MAR-1996.
 XX 22-SEP-1995; 95WO-US12080.
 XX 22-SEP-1994; 94US-0310722.
 XX {CHIL-} CHILDRENS MEDICAL CENT.
 XX Bernfield M, Gallo RL;
 XX WPI; 1996-188401/19.
 XX Modulating mesenchymal interaction by administration of syndecan -
 PT used in the treatment of wounds, tumours, restenosis, etc
 XX
 XX Claim 4; Page 26; 34pp; English.

CC The present peptide is a syndecan, which induces the expression of
 CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
 CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of
 CC the peptide were found to be identical to the 36 N-terminal amino
 CC acids of PR-39, a Pro and Arg rich antibacterial peptide previously
 CC found in porcine intestine (W09222578). Syndecins may be used in
 CC the treatment of stasis and decubitus ulcers, keloids, skin burns,
 CC ischemic tissues and hypercoagulation states, prevention of tumour
 CC metastasis, restenosis inhibition and endothelial cell angiogenesis
 CC and proliferation induction.
 CC Human microvascular endothelial cells were assayed for syndecan-4
 CC expression following exposure to 5 % wound fluid, dbcAMP (1 mM).
 CC the present peptide (10 microm) or a blank, to give respective
 CC cell surface syndecan-4 values (MOD/m in) of approx. 1.75, 1.70,
 CC 1.80 and 0.95.

XX SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 17; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPPPYLPFRPP 15
 |||||
 DB 1 RRRPPPYLPFRPP 15

RESULT 10
 AAR99121
 ID AAR99121 standard; peptide; 39 AA.

XX AAR99121;
 XX
 XX 28-OCT-1996 (first entry)
 XX
 XX Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
 XX STD; sexually transmitted disease; HIV; human immunodeficiency virus;
 XX herpes simplex virus; HSV; Neisseria gonorrhoeae; Candida; Chlamydia;
 XX magainin; antimicrobial; squalamine.

XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 39
 XX FT /note= "amidated"

XX W09608270-A2.
 XX 21-MAR-1996.
 XX 13-SEP-1995; 95WO-US11675.
 XX 13-SEP-1994; 94US-0305475.
 XX (MAGA-) MAGAININ PHARM INC.

XX Bedi G, Jacob L, Williams T, Zasloff M;
 XX WPI; 1996-179725/18.

XX Inhibiting sexually transmitted disease e.g. HIV or herpes simplex -
 PT by administering magainin antimicrobial or squalamine cpd. to
 PT inhibit transmission

XX Example 1; Page 32; 60pp; English.

XX AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may
 CC be used to treat sexually transmitted diseases (STDs) caused by
 CC Chlamydia, HIV, herpes simplex virus, Neisseria gonorrhoeae or
 CC Candida infection. The peptides inhibit STDs by either killing the
 CC infectious organism, impeding the infection mechanism or
 CC interrupting the replication cycle of the organism. Squalamine (an

CC aminosterol host defence molecule of the dog fish shark *Squalus*
 CC acanthias) and pGLa (a frog antimicrobial peptide) analogues may
 CC also be useful in inhibiting STD infection and transmission.

XX Sequence 39 AA;
 SQ Query Match 100.0%; Score 90; DB 17; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 11
 AAW75722
 ID AAW75722 standard; peptide; 39 AA.
 XX
 AC AAW75722;
 XX
 DT 19-NOV-1998 (first entry)
 XX
 DE Proline/Arginine rich peptide PR-39.
 XX
 KW Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
 KW superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
 KW coronary bypass; organ transplantation surgery.
 XX
 OS Synthetic.
 XX
 PN WO9835690-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 17-FEB-1998; 98WO-US03207.
 XX
 PR 16-FEB-1998; 98US-0024975.
 PR 18-FEB-1997; 97US-0802306.
 XX
 PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 XX Blecha P, Ross CR, Shi J;
 PI WPI; 1998-495359/42.
 DR
 XX Reduction of reperfusion injury in temporarily occluded blood
 PT vessels - by administration of a peptide which is rich in proline
 PT or arginine residues
 XX
 PS Claim 3; Page 14; 35pp; English.

XX Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
 CC administration into a mammal's bloodstream reduce reperfusion injury
 CC (production of reactive oxygen species, neutrophil adherence to
 CC endothelium, and extravasation of neutrophils). These peptides have two
 CC requirements: they contain the consensus sequence PXXP, where P is a
 CC proline residue and X is any amino acid residue, which has been found to
 CC inhibit superoxide production, and secondly they have arginine residues
 CC adjacent to these motifs, required for effective inhibition. It was
 CC established by structural and function analysis that a peptide should
 CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
 CC correlated with the increase of length of peptides. The effectiveness
 CC of these peptides was determined by investigating the production of the
 CC neutrophil superoxide anion, and also the inhibition of neutrophil
 CC chemotaxis. From this, it was found that all of the peptides inhibited
 CC NADPH oxidase to some extent. All of the peptides also inhibit
 CC neutrophil oxidase activity. PR-39 is believed, to be the most potent
 CC endogenous down regulator of NADPH oxidase yet discovered, and from the
 CC data produced, it can be suggested to be involved in eliminating or
 CC reducing the reperfusion injury induced adhesion and extraction of
 CC neutrophils. The peptides are also useful in connection with surgical
 CC procedures such as coronary bypass and organ transplantation surgery.

XX Sequence 39 AA;
 SQ Query Match 100.0%; Score 90; DB 19; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 12
 AAB26888
 ID AAB26888 standard; peptide; 39 AA.
 XX
 AC AAB26888;
 XX
 DT 01-FEB-2001 (first entry)
 XX
 DE PR-39 peptide used in angiogenesis control.
 XX
 KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
 KW myocardial ischaemia; proteasome.
 XX
 OS Synthetic.
 XX
 PN WO200057895-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 16-MAR-2000; 2000WO-US07050.
 XX
 PR 26-MAR-1999; 99US-0276868.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 XX Simons M, Gao Y;
 PI WPI; 2000-628319/60.
 DR
 XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
 PT infarction, by administering a PR-39 oligopeptide that regulates
 PT enzymatic activity of proteasomes -
 XX
 PS Disclosure; Page 21; 51pp; English.

XX This invention relates to a method for the stimulation of angiogenesis in
 CC situ within a targeted collection of viable cells. The method comprises
 CC introducing into the cytoplasm, at least 1 member of the PR-39
 CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
 CC Part of the proteolytic activity of the proteasomes is selectively
 CC altered so as to stimulate angiogenesis. The method is used to induce
 CC angiogenesis in tissue that has suffered anoxia or infarction, and also to
 CC e.g. myocardial infarction or chronic myocardial ischaemia, and also to
 CC study the mechanisms that control angiogenesis. The present sequence
 CC represents the PR-39 peptide from which peptide used in the method of
 CC the invention are derived.

XX Sequence 39 AA;
 SQ Query Match 100.0%; Score 90; DB 21; Length 39;
 Best Local Similarity 100.0%; Pred. No. 0.00055;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRRPP 15
 DB 1 RRRPRPPYLPRRPP 15

RESULT 13
 AAB84690
 ID AAB84690 standard; protein; 39 AA.

Tue Jul 6 16:40:31 2004

XX AC AAB84690;
XX DT 17-SEP-2001 (first entry)
XX DE Amino acid sequence of a PR-39 protein.
XX KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
XX KW myocardial infarction; chronic myocardial ischemia; heart disease;
XX KW anoxia.
XX OS Unidentified.
XX PN WO200147540-A1.
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-US35293.
XX PR 29-DEC-1999; 99US-0474967.
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PI Simons M, Gao Y;
XX DR WPI; 2001-441690/47.
XX CC Selective inhibition of IkappaBalpha degradation within targeted viable
XX CC cell collection, involves interacting PR-39 oligopeptide with
XX CC IkappaBalpha and proteasomes, and altering proteolytic activity of
XX CC proteasomes -
XX PS Disclosure; Page 30; 69pp; English.
XX CC The present sequence represents a PR-39 protein. The specification
XX CC describes PR-39 derived peptides, which are used for selective
XX CC inhibition of IkappaBalpha degradation within a targeted cell collection
XX CC in-situ. The method is useful for selectively inhibiting IkappaBalpha
XX CC protein degradation in situ, decreasing the activity of NFkappaB
XX CC transcription factor and selective control of NFkappaB-dependent gene
XX CC expression in situ. The PR-39 derived peptides are useful in the
XX CC treatment of myocardial infarction, chronic myocardial ischemia of
XX CC heart disease and anoxia.
XX SQ Sequence 39 AA;
Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00055;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPRPPVLP RPRPP 15
Db 1 RRRPRPPVLP RPRPP 15
RESULT 14
AAB97280
ID AAB97280 standard; peptide; 39 AA.
XX AC AAB97280;
XX DT 09-AUG-2001 (first entry)
XX DE PR-39 peptide.
XX KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;
XX KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
XX KW anoxia; chronic myocardial ischemia; heart tissue.
XX OS Unidentified.
XX PN WO200130368-A1.
XX PR 17-AUG-2000; 2000AT-0001416.

PD XX 03-MAY-2001.
XX PF 06-OCT-2000; 2000WO-US27552.
XX PR 25-OCT-1999; 99US-0426011.
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PI Simons M, Gao Y;
XX DR WPI; 2001-355179/37.
XX CC Stimulation of angiogenesis and inhibition of proteasome mediated
XX CC degradation in cells, by introduction of PR-39 oligopeptide or its
XX CC N-terminal fragments or their conjugates, for use in anoxia and
XX CC infarction conditions -
XX PS Disclosure; Page 21; 52pp; English.
XX CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
XX CC is a member of the cathelin family of proteins, mature PR-39
XX CC represented by the present sequence is 39 amino acids in length, and has
XX CC been shown to play a role in several inflammatory events including wound
XX CC healing and myocardial infarction. The PR-39 derived family of
XX CC oligopeptides cause selective inhibition of proteasome mediated
XX CC degradation of peptides and stimulation of angiogenesis after their
XX CC intracellular introduction to a target cell. PR-39 derived peptides are
XX CC able to interact with at least the alpha7 subunit of the proteasomes, and
XX CC therefore alter the proteolytic activity of proteasomes such that a
XX CC selective increased expression of specific proteins occurs. The invention
XX CC includes methods for the selective inhibition of proteasome mediated
XX CC peptide degradation. The method provides means for stimulating
XX CC angiogenesis as required in living tissues and organs which have suffered
XX CC defects or have undergone anoxia and/or infarction, myocardial infarction
XX CC or chronic myocardial ischemia of heart tissue. Examples are the
XX CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,
XX CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and
XX CC extremities. A particular example is after myocardial infarction or
XX CC ischaemia.
XX SQ Sequence 39 AA;
Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00055;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRRPRPPVLP RPRPP 15
Db 1 RRRPRPPVLP RPRPP 15
RESULT 15
ABB07714
ID ABB07714 standard; peptide; 42 AA.
XX AC ABB07714;
XX DT 10-JUN-2002 (first entry)
XX DB Antimicrobial peptide PR-39 C-terminal fragment.
XX KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
XX KW antigen presenting cell; adjuvant; porcine; PR-39.
XX OS Sus sp.
XX PN WO200213857-A2.
XX PD 21-FEB-2002.
XX PF 17-AUG-2001; 2001WO-EP09529.
XX PR 17-AUG-2000; 2000AT-0001416.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMEH.
PA Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
XX WPI; 2002-269154/31.
XX
XX Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at
PT least one antigen and at least one cathelicidin derived antimicrobial
PT peptide -
XX
XX Disclosure; Fig 3; 65pp; English.
XX
XX The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences BB07708-15 represent C-terminal fragments of antimicrobial
CC peptides of the cathelicidin family.
XX
SQ Sequence 42 AA;
Query Match 100.0%; Score 90; DB 23; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPRPPYLPFRPP 15
Db 1 RRRPRPPYLPFRPP 15

Search completed: October 1, 2003, 19:03:11
Job time : 83 secs

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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:01:53 ; Search time 29 Seconds
(without alignments)
21.885 Million cell updates/sec

Title: US-09-426-01ld-3

Perfect score: 90
Sequence: 1 RRRPRPPLPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	26	2	US-08-419-066-2
2	90	100.0	26	3	US-09-024-975-2
3	90	100.0	39	1	US-08-162-052-1
4	90	100.0	39	1	US-08-310-722-1
5	90	100.0	39	2	US-08-419-066-1
6	90	100.0	39	2	US-08-728-333-1
7	90	100.0	39	3	US-09-024-975-1
8	90	100.0	39	5	PCT-US95-12080-1
9	83	92.2	14	3	US-09-024-975-4
10	66	73.3	20	3	US-09-024-975-9
11	66	73.3	59	4	US-09-030-619-163
12	61	67.8	336	1	US-08-414-926A-26
13	61	67.8	336	2	US-08-926-922-26
14	61	67.8	336	3	US-09-283-682-26
15	61	67.8	336	3	US-09-527-657-26
16	59	65.6	59	5	PCT-US95-12080-3
17	55	61.1	93	4	US-09-252-991A-29133
18	55	61.1	311	4	US-09-252-991A-22406
19	54.5	60.6	425	4	US-09-252-991A-19054
20	54	60.0	594	4	US-09-252-991A-32578
21	53	58.9	18	1	US-08-205-938A-23
22	53	58.9	18	1	US-08-205-938A-24
23	53	58.9	18	3	US-09-230-180-26
24	53	58.9	18	4	US-09-030-619-96
25	53	58.9	18	4	US-09-030-619-158
26	53	58.9	18	4	US-09-030-619-159
27	53	58.9	18	5	PCT-US95-02626-23

Sequence 24, Appl
Sequence 6408, Ap
Sequence 25, Appl
Sequence 160, App
Sequence 25, Appl
Sequence 26492, A
Sequence 41, Appl
Sequence 41, Appl
Sequence 3, Appl
Sequence 29050, A
Sequence 8, Appl
Sequence 21389, A
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 17939, A

28 53 58.9 18 5 PCT-US95-02626-24
29 52.5 58.3 129 4 US-09-328-353-6408
30 52 57.8 18 1 US-08-205-938A-25
31 52 57.8 18 4 US-09-030-619-160
32 52 57.8 18 5 PCT-US95-02626-25
33 52 57.8 144 4 US-09-252-991A-26492
34 51.5 57.2 355 3 US-08-483-533-41
35 51.5 57.2 355 4 US-09-283-471A-41
36 51.5 57.2 355 5 PCT-US91-06532-3
37 51.5 57.2 381 4 US-09-252-991A-29050
38 51 56.7 16 1 US-08-205-938A-8
39 51 56.7 16 5 PCT-US95-02626-8
40 51 56.7 159 4 US-09-252-991A-21389
41 51 56.7 180 3 US-09-187-331-5
42 51 56.7 180 4 US-09-470-946-5
43 51 56.7 195 3 US-09-187-331-1
44 51 56.7 195 4 US-09-470-946-1
45 51 56.7 263 4 US-09-252-991A-17939

ALIGNMENTS

RESULT 1
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 100.0%; Score 90; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e-05; 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0;
QY 1 RRRPRPPLPRPP 15

Db 1 RRRPPPYLPRPP 15

RESULT 2

US-09-024-975-2
; Sequence 1, Application US/09024975
; Patent No. 6133233
; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 100.0%; Score 90; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPYLPRPP 15
Db 1 RRRPPPYLPRPP 15

RESULT 3

US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong-Youn
; APPLICANT: BOMAN, Hans G
; APPLICANT: MUTT, Viktor
; APPLICANT: JORNVAL, Hans
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92-22578
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 0033000-299
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-162-052-1

Query Match 100.0%; Score 90; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPPYLPRPP 15
Db 1 RRRPPPYLPRPP 15

RESULT 4

US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508

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TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jorvall, Hans
TITLE: No. 5654273ed Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match 100.0%; Score 90; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. NO. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPP 15
Db 1 RRRPRPPYLP RPP 15

RESULT 5
US-08-419-066-1
Sequence 1, Application US/08419066
Patent No. 5830993
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
APPLICANT: Shi, Jishu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
ADDRESSEE: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Cgllins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-419-066-1

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LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-4

Query Match 92.2%; Score 83; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPPYLPYLPYLP 14
Db 1 RRRPPYLPYLPYLP 14

RESULT 10

US-09-024-975-9
Sequence 9, Application US/09024975
Patent No. 6133233
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-9

Query Match 73.3%; Score 66; DB 3; Length 20;
Best Local Similarity 85.7%; Pred. No. 0.041;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRRPPYLPYLPYLP 14
Db 2 RIRPPYLPYLPYLP 15

RESULT 11

US-09-030-619-163
Sequence 163, Application US/09030619B
Patent No. 6503881
GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 66081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 163
LENGTH: 59
TYPE: PRT
ORGANISM: Bos taurus
US-09-030-619-163

Query Match 73.3%; Score 66; DB 4; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.11;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRRPPYLPYLPYLP 14
Db 2 RIRPPYLPYLPYLP 15

RESULT 12

US-08-414-926A-26
Sequence 26, Application US/08414926A
Patent No. 5721354
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/414,926A
FILING DATE: March 31, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR-011/COUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tel.22
FEATURE:
NAME/KEY: Protein
LOCATION: 1..336
OTHER INFORMATION: /label= U0151

US-08-414-926A-26

Query Match 67.8%; Score 61; DB 1; Length 336;
 Best Local Similarity 78.6%; Pred. No. 2.1;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPPLPRPP 15
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 Db 279 RRPPLPRPP 292

RESULT 13

US-08-926-922-26
 ; Sequence 26, Application US/08926922
 ; Patent No. 5925751

; GENERAL INFORMATION:
 ; APPLICANT: Spaete, Richard
 ; APPLICANT: Cha, Tai-An
 ; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Luann Cserr Attorney at Law
 ; STREET: 750 Arimo Avenue
 ; CITY: Oakland
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94610

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/926,922
 ; FILING DATE: September 10, 1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cserr, Luann
 ; REGISTRATION NUMBER: 31,822
 ; REFERENCE/DOCKET NUMBER: AVIR 11A

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 510-834-1448
 ; TELEFAX: 510-839-7810
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 336 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; IMMEDIATE SOURCE:
 ; CLONE: tol.22
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..336
 ; OTHER INFORMATION: /label= UL151

US-08-926-922-26
 ; Query Match 67.8%; Score 61; DB 2; Length 336;
 ; Best Local Similarity 78.6%; Pred. No. 2.1;
 ; Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPPLPRPP 15
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 Db 279 RRPPLPRPP 292

RESULT 14

US-09-253-682-26
 ; Sequence 26, Application US/09253682
 ; Patent No. 6040170

; GENERAL INFORMATION:
 ; APPLICANT: Spaete, Richard
 ; APPLICANT: Cha, Tai-An

; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
 ; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Luann Cserr Attorney at Law
 ; STREET: 750 Arimo Avenue
 ; CITY: Oakland
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94610

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/253,682
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/926,922
 ; FILING DATE: September 10, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cserr, Luann
 ; REGISTRATION NUMBER: 31,822
 ; REFERENCE/DOCKET NUMBER: AVIR 11A

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 510-834-1448
 ; TELEFAX: 510-839-7810
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 336 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; IMMEDIATE SOURCE:
 ; CLONE: tol.22
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..336
 ; OTHER INFORMATION: /label= UL151

US-09-253-682-26
 ; Query Match 67.8%; Score 61; DB 3; Length 336;
 ; Best Local Similarity 78.6%; Pred. No. 2.1;
 ; Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPPLPRPP 15
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 Db 279 RRPPLPRPP 292

RESULT 15

US-09-527-657-26
 ; Sequence 26, Application US/09527657
 ; Patent No. 6291236

; GENERAL INFORMATION:
 ; APPLICANT: Spaete, Richard
 ; APPLICANT: Cha, Tai-An
 ; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Luann Cserr Attorney at Law
 ; STREET: 750 Arimo Avenue
 ; CITY: Oakland
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94610

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/527,657
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-527-657-26

Query Match      67.8%; Score 61; DB 3; Length 336;
Best Local Similarity 78.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 RRPRPPYLPRPRPP 15
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Db      279 RRPPIPLQPRPP 292

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Search completed: October 1, 2003, 19:06:44
 Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:03:18 ; Search time 27 seconds
(without alignments)
87.896 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPRPVLPFRPP 15

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	83	92.2	14	15	US-10-014-147-7
5	75	83.3	23	15	US-10-014-147-3
6	66	73.3	59	9	US-09-030-619-163
7	60	66.7	953	9	US-09-888-615-66
8	56.5	62.8	74	9	US-09-864-761-45555
9	55	61.1	45	9	US-09-864-761-49065
10	55	61.1	273	15	US-10-156-761-8265
11	54	60.0	250	15	US-10-103-806-517
12	53	58.9	18	9	US-09-030-619-96
13	53	58.9	18	9	US-09-030-619-158
14	53	58.9	18	9	US-09-030-619-159
15	53	58.9	18	12	US-10-229-368-1

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Sequence 4, Appli
Sequence 160, Appl
Sequence 14520, A
Sequence 2, Appli
Sequence 58, Appli
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Sequence 13550, A
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Sequence 13, Appli
Sequence 20, Appli
Sequence 29, Appli
Sequence 21, Appli
Sequence 35, Appli
Sequence 237, App
Sequence 2258, Ap
Sequence 320, App
Sequence 643, App
Sequence 320, App
Sequence 438, App
Sequence 97, Appl
Sequence 7617, Ap
Sequence 204, App

16 53 58.9 18 12 US-10-225-087-1
17 53 58.9 18 15 US-10-181-654-4
18 52 57.8 18 9 US-09-030-619-160
19 52 57.8 260 15 US-10-156-761-14520
20 52 57.8 354 14 US-10-004-717-2
21 52 57.8 354 14 US-10-004-717-58
22 51 56.7 180 10 US-09-997-701-5
23 51 56.7 195 10 US-09-997-701-1
24 51 56.7 235 15 US-10-153-668-59
25 50.5 56.1 304 15 US-10-156-761-13550
26 50.5 56.1 392 10 US-09-747-835A-55
27 50.5 56.1 393 15 US-10-243-035-2
28 50.5 56.1 419 9 US-09-828-035-2
29 50.5 56.1 419 12 US-10-345-680-44
30 50.5 56.1 419 12 US-10-146-733-29
31 50.5 56.1 1122 12 US-10-188-869-13
32 50.5 56.1 1145 12 US-10-188-869-20
33 50.5 56.1 1314 10 US-09-747-835A-29
34 50 55.6 18 15 US-10-181-654-21
35 50 55.6 18 15 US-10-181-654-35
36 50 55.6 99 9 US-09-864-761-43778
37 50 55.6 146 10 US-09-989-920-237
38 50 55.6 327 12 US-10-017-161-2258
39 50 55.6 449 9 US-09-764-870-320
40 50 55.6 449 9 US-09-764-853-643
41 50 55.6 449 15 US-10-135-540-320
42 50 55.6 449 15 US-10-103-313-438
43 49.5 55.0 129 11 US-09-975-719-97
44 49.5 55.0 156 15 US-10-156-761-7617
45 49 54.4 223 14 US-10-052-254-204

ALIGNMENTS

RESULT 1
US-10-014-147-4
; Sequence 4, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/014,147
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,777A
; FILING DATE: October 8, 1997
; APPLICATION NUMBER: PCT/US96/04674
; FILING DATE: April 10, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 23625-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-014-147-4

Query Match 100.0%; Score 90; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPFRPP 15
Db 1 RRRPRPPYLPFRPP 15

RESULT 2

US-10-014-147-2
; Sequence 2, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-014-147-2

Query Match 100.0%; Score 90; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPFRPP 15
Db 1 RRRPRPPYLPFRPP 15

RESULT 3

US-10-014-147-1
; Sequence 1, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-147-1

Query Match 100.0%; Score 90; DB 15; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPFRPP 15
Db 1 RRRPRPPYLPFRPP 15

RESULT 4

US-10-014-147-7
; Sequence 7, Application US/10014147
; Publication No. US20030125249A1
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; Shi, Jishu
; TITLE OF INVENTION: Synthetic Antimicrobial Peptide
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Blvd., Ste. 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCES/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-014-147-7
Query Match 92.2%; Score 83; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRRPPPPYLP RRP 14
DB 1 RRRPPPPYLP RRP 14
RESULT 5
US-10-014-147-3
Sequence 3, Application US/10014147
Publication No. US20030125249A1
GENERAL INFORMATION:
APPLICANT: Blecha, Frank
TITLE OF INVENTION: Synthetic Antimicrobial Peptide
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Williams, Timmons & Collins
STREET: 2405 Grand Blvd., Ste. 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,147
FILING DATE: 07-Dec-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/930,777A
FILING DATE: October 8, 1997
APPLICATION NUMBER: PCT/US96/04674
FILING DATE: April 10, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCES/DOCKET NUMBER: 23625-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-014-147-3
Query Match 83.3%; Score 75; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PRPPYLP RRP 15
DB 1 PRPPYLP RRP 12
RESULT 6
US-09-030-619-163
Sequence 163, Application US/09030619B
Patent No. US20020035061A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 163
LENGTH: 59
TYPE: PRT
ORGANISM: Bos taurus
US-09-030-619-163
Query Match 73.3%; Score 66; DB 9; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.96;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RRRPPPPYLP RRP 14
DB 2 RRRPPPPYLP RRP 15
RESULT 7
US-09-888-615-66
Sequence 66, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: FLOWMAN, GREGORY
APPLICANT: WHITE, DAVID
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 953

TYPE: PRT
ORGANISM: Homo sapiens
US-09-888-615-66

Query Match 66.7%; Score 60; DB 9; Length 953;
Best Local Similarity 56.5%; Pred. No. 42;
Matches 13; Conservative 0; Mismatches 2; Indels 8; Gaps 1;

QY 1 RRRPRP-----PYLPRPP 15
||||| :|||
Db 377 RRRPRPOTRLTTPQPRPP 399

RESULT 3

US-09-864-761-45555
; Sequence 45555, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45555

LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: MAP TO AC010458.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EST_HUMAN HIT: AWS83858.1, EVALUATE 5.00e-20
US-09-864-761-45555

Query Match 62.8%; Score 56.5; DB 9; Length 74;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 9; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRPRPPY-LPRPP 15
||||| :|||
Db 37 RRRPRPPRIPEKPP 52

RESULT 9

US-09-864-761-49065
; Sequence 49065, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 49065

LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

; OTHER INFORMATION: MAP TO AC005973.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.88
; OTHER INFORMATION: EST_HUMAN HIT: A1358103.1, EVALUATE 4.60e+00
US-09-864-761-49065

Query Match 61.1%; Score 55; DB 9; Length 45;
Best Local Similarity 76.9%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPR 13
||| ||| |||
Db 19 RRRPRPPGPRPQ 31

RESULT 10

US-10-156-761-8265
; Sequence 8265, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8265
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8265

Query Match 61.1%; Score 55; DB 15; Length 273;
Best Local Similarity 70.6%; Pred. No. 51;
Matches 12; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 RRRPRPPYLP-RPRPP 15
||| ||| |||
Db 224 RRRPRPPRPGSRPRHP 240

RESULT 11

US-10-102-806-517
; Sequence 517, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 517
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: SITE
; LOCATION: (118)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (1161)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (204)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-517

Query Match 60.0%; Score 54; DB 15; Length 250;
Best Local Similarity 71.4%; Pred. No. 61;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPR 14
||| ||| |||
Db 202 RRRPRPPAARPRP 215

RESULT 12

US-09-030-619-96
; Sequence 96, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 96
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-96

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLP RPRPP 15
||| ||| |||
Db 4 RPVYLPQPRPP 14

RESULT 13

US-09-030-619-158
; Sequence 158, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25

; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-030-619-158

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RPPYLPQPRPP 15
Db 4 RPYVLPQPRPP 14

RESULT 14

US-09-030-619-159
; Sequence 159, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 159
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Apis mellifera
US-09-030-619-159

Query Match 58.9%; Score 53; DB 9; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RPPYLPQPRPP 15
Db 4 RPYVLPQPRPP 14

RESULT 15

US-10-229-368-1
; Sequence 1, Application US/10229368
; Publication No. US20030148945A1
; GENERAL INFORMATION:
; APPLICANT: McNicol, Patricia J.
; APPLICANT: Pawlak, Sonia K.
; APPLICANT: Rubinchik, Evelina
; APPLICANT: Cameron, Dale
; APPLICANT: Guarna, Maria Marta
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 660081.418
; CURRENT APPLICATION NUMBER: US/10/229,368
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Indolicidin peptide analogs
US-10-229-368-1

Query Match 58.9%; Score 53; DB 12; Length 18;
Best Local Similarity 72.7%; Pred. No. 8.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 RPPYLPQPRPP 15
Db 4 RPYVLPQPRPP 14

Search completed: October 1, 2003, 19:07:18
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:00:33 ; Search time 39 Seconds
(without alignments)
36.988 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPRPPYLRPRPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	172	2	S68232
2	66	73.3	59	2	antimicrobial prot
3	59.5	66.1	82	2	bactescin 7 - bov
4	58	64.4	190	2	spore coat protein
5	56.5	62.8	168	2	antimicrobial pept
6	56.5	62.8	199	2	apidaecin 14 precu
7	55	61.1	437	2	extensin class I (
8	54.5	60.6	301	2	protein R3D11.3 (
9	54	60.0	359	2	hybrid proline-rich
10	54	60.0	427	2	hypothetical prote
11	53	58.9	26	2	apidaecin 1b precu
12	53	58.9	144	2	apidaecin 22 precu
13	53	58.9	184	2	hypothetical prote
14	53	58.9	283	2	apidaecin 73 precu
15	53	58.9	428	2	probable coll wall
16	53	58.9	491	2	proline-rich prot
17	52	57.8	261	1	infected cell prot
18	52	57.8	439	2	chitinase (EC 3.2.
19	52	57.8	467	2	protein kinase, 54
20	52	57.8	1006	2	hypothetical prote
21	51.5	57.2	1187	1	protein-tyrosine-p
22	51.5	57.2	1189	1	protein-tyrosine-p
23	51	56.7	180	2	PBX protein - hum
24	50.5	56.1	1216	2	synaptotagmin 2 alp
25	50	55.6	192	2	hypothetical prote
26	50	55.6	383	2	zinc finger protei
27	50	55.6	415	1	acrosin (EC 3.4.21
28	50	55.6	421	2	acrosin (EC 3.4.21
29	50	55.6	424	2	spliceosome-associ

30 50 55.6 449 2 S16748
31 50 55.6 547 2 C96828
32 50 55.6 1460 1 EBBE1F
33 50 55.6 3036 2 T18995
34 49.5 55.0 589 2 T29299
35 49 54.4 118 2 T19345
36 49 54.4 134 2 JC5572
37 49 54.4 161 2 T72593
38 49 54.4 210 2 T33700
39 49 54.4 218 2 T22261
40 49 54.4 296 2 A27319
41 49 54.4 296 2 S07361
42 49 54.4 352 2 F84799
43 49 54.4 369 2 S20500
44 49 54.4 380 2 T32944
45 49 54.4 413 2 H87604

ALIGNMENTS

RESULT 1

S68232 antimicrobial protein PR-39 precursor, cathelin-associated - pig

N:Alternate names: myeloid antibacterial protein PR-39

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68232; JN0899; I47138; S19563

R:Zhao, C.; Ganz, T.; Lehrer, R.I.

FEBS Lett. 376, 130-134, 1995

A:Title: Structure of genes for two cathelin-associated antimicrobial peptides: proph

A:Reference number: S68232; MUID:96105365; PMID:7498526

A:Accession: S68232

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-172 <ZHA>

A:Cross-references: EMBL:X89201; NID:gl165150; PIDN:CAA61487.1; PID:gl165151

A:Experimental source: leukocytes

R:Storici, P.; Zanetti, M.

Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993

A:Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to th

A:Reference number: JN0899; MUID:94071853; PMID:8250863

A:Accession: JN0899

A:Molecule type: mRNA

A:Residues: 1-20, 'A', 22-172 <STO>

A:Cross-references: GB:I23825; NID:g435100; PIDN:AAA31109.1; PID:g435101

A:Experimental source: bone marrow cells

R:Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; B

Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995

A:Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene f

A:Reference number: I47138; MUID:95350216; PMID:7624374

A:Accession: I47138

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-28, 'T', 30-89, 'QR', 92-116, 'NDP', 120-172 <GUD>

A:Cross-references: EMBL:X87236; NID:9829142; PIDN:CAAG0682.1; PID:gl051298

R:Agarberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernva

Eur. J. Biochem. 202, 849-854, 1991

A:Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of

A:Reference number: S19563; MUID:92111534; PMID:1765098

A:Accession: S19563

A:Molecule type: protein

A:Residues: 131-169 <AGE>

A:Experimental source: intestine

C:Genetics:

A:Gene: PR39

A:Introns: 66/3; 102/3; 126/3

C:Superfamily: cathelin; cystatin homology

C:Keywords: amidated carboxyl end; antibacterial

F:1-29/Domain: signal sequence #status Predicted <SIG>

F:22-129/Domain: cystatin homology <Cys>

F:30-130/Domain: propeptide #status Predicted <PRO>

F:131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

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Query Match          100.0%; Score 90; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      1 RRRPRPPYLPRRPP 15  
        |||||            |||||  
DB     131 RRRPRPPYLPRRPP 145  
  
RESULT 2  
A:Accession: A36589  
A:Species: Bos primigenius taurus (cattle)  
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997  
C:Accession: A36589  
R:Frank, R.W.; Genaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.  
J. Biol. Chem. 265, 18871-18874, 1990  
A:Title: Amino acid sequences of two proline-rich bactericins. Antimicrobial peptides of  
A:Reference number: A36589; PMID:91035404; PMID:2229048  
A:Accession: A36589  
O  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-59 <PRA>  
C:Superfamily: cathelin; cystatin homology  
  
Query Match          73.3%; Score 66; DB 2; Length 59;  
Best Local Similarity 85.7%; Pred. No. 0.087;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY      1 RRRPRPPYLPRRP 14  
        |||||           |||||  
DB      2 RIRPRPRLPRLRP 15  
  
RESULT 3  
A41051  
spore coat protein precursor - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 03-Apr-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2002  
C:Accession: S04835; A41051; F69606  
R:Aranson, A.I.; Song, H.Y.; Bourne, N.  
Mol. Microbiol. 3, 437-444, 1989  
A:Title: Gene structure and precursor processing of a novel Bacillus subtilis spore coat  
A:Reference number: S04835; PMID:89313296; PMID:2546006  
A:Accession: S04835  
A:Molecule type: DNA  
A:Residues: MNVTFNLSTRNWVGKIKAREVELL, 2-82 <AR2>  
A:Cross-references: EMBL:X131740; NID:S93964; PIDN:CA32004.1; PID:g39865  
A:Experimental source: strain JH642  
A>Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Bourne, N.; FitzJames, P.C.; Aronson, A.I.  
J. Bacteriol. 173, 6618-6625, 1991  
A:Title: Structural and germination defects of Bacillus subtilis spores with altered con  
A:Reference number: A41051; PMID:92011439; PMID:1917883  
A:Accession: A41051  
A:Molecule type: protein  
A:Residues: 'XX', 3-11 <BOU>  
A:Experimental source: strain JH642  
A>Note: the material sequenced was the larger of two isolated precursor forms, the amino  
A>Note: both the location of the transcription start site and peptide sequencing of the  
R:Kunst, P.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.P.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinio  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel  
Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetello  
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
Thabba, M.; Schleibach, S.; Schuster, P.; Scorrone, P.; Sekowska, A.; Seron  
A:
```

Query Match 66.1%; Score 59.5; DB 2; Length 82;
Best Local Similarity 84.6%; Pred. No. 0.7; 1; Indels 1; Gaps 1;
Matches 11; Conservative 0; Mismatches 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 PRPP-YLPRPRPP 15
| | | | | | | | | |
DB 49 PRPPYYPRPP 61

RESULT 4
S68230
antimicrobial peptide precursor - sheep
N:Alternate names: Bac7.5 peptide homolog
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S68230
R:Bagella, L.; Scocchi, M.; Zanetti, M.
FEBS Lett. 376, 225-228, 1995
A:Title: cDNA sequences of three sheep myeloid cathelicidins.
A:Reference number: S68228; MUID:96105386; PMID:7498547
A:Accession: S68230
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-190 <BAG>
A:Cross-references: EMBL:L46852; NID:gl161244; PIDN:AAA85468.1; PID:gl161245
C:Superfamily: cathelin; cystatin homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:22-129/Domain: cystatin homology <YS>
F:29-130/Domain: propeptide #status predicted <PRO>
F:130-190/Product: antimicrobial peptide #status predicted <MAT>

Query Match 64.4%; Score 58; DB 2; Length 190;
Best Local Similarity 78.6%; Pred. No. 2.4;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRPP 14
| | | | | | | | | |
DB 132 RLRRPRRLPRPP 145

RESULT 5
S35330
apidaecin 14 precursor - honeybee
N:Contains: apidaecin II
C:Species: Apis mellifera (honeybee)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S35330; S06676
R:Casteele-Josson, K.; Capaci, T.; Casteele, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A:Title: Apidaecin multipitptide precursor structure: a putative mechanism for amplification
A:Reference number: S35330; MUID:93223897; PMID:8467807
A:Accession: S35330
A:Molecule type: mRNA
A:Residues: 1-168 <CAS>

A;Residues: 1-427 <CHI>
A;Cross-references: EMBL:AF039043; PIDN:AA94196.1; GSPDB:GN00028; CESP:F39C12.3
A;Experimental source: strain Bristol N2; clone F39C12
C;Genetics:
A;Gene: CESP:F39C12.3
A;Map position: X
A;Introns: 42/3; 104/3; 133/3; 164/3; 213/3; 276/3; 336/3

Query Match 60.0%; Score 54; DB 2; Length 427;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RPPYLPRLPRPP 15
|||:|:|:|
DB 338 RPPDPDIPPLPP 350

RESULT 11

S06675

apidaecin 1b precursor - honeybee

C;Species: Apis mellifera (honeybee)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Dec-1998

A;Accession: S06675

R;Casteels-Josson, P.; Ampe, C.; Jacobs, P.; Vaack, M.; Tempst, P.

EMBO J. 8, 2387-2391, 1989

A;Title: Apidaecins: antibacterial peptides from honeybees.

A;Reference number: S05383; MUID:90005446; PMID:2676519

A;Accession: S06675

A;Molecule type: protein

A;Residues: 1-26 <CAS>

F;1-8/Domain: propeptide #status experimental <PRO>

F;9-26/Product: apidaecin 1b #status experimental <MAT>

Query Match 58.9%; Score 53; DB 2; Length 26;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
|||:|:|:|
DB 12 RPVIQPRPP 22

RESULT 12

S35331

apidaecin 22 precursor - honeybee

C;Species: Apis mellifera (honeybee)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

A;Accession: S35331

R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.

EMBO J. 12, 1569-1578, 1993

A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplifica

A;Reference number: S35330; MUID:93223697; PMID:8467807

A;Accession: S35331

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-144 <CAS>

A;Cross-references: EMBL:X72576; NID:9297064; PIDN:CAA51168.1; PID:g297065

C;Superfamily: procyclic acidic repetitive protein

Query Match 58.9%; Score 53; DB 2; Length 144;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
|||:|:|:|
DB 46 RPVIQPRPP 56

RESULT 13

T29373

hypothetical protein ZC404.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C;Accession: T29373
R;Bentley, D.; Le, T.T.
Submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid ZC404.
A;Reference number: Z20614
A;Accession: T29373
A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-184 <BEN>

A;Cross-references: EMBL:U55363; PIDN:AAA97967.1; GSPDB:GN00023; CESP:ZC404.1

A;Experimental source: strain Bristol N2; clone ZC404

C;Genetics:

A;Gene: CESP:ZC404.1

A;Map position: 5

A;Introns: 15/2; 50/2; 75/2; 138/2

C;Superfamily: Caenorhabditis elegans hypothetical protein ZC404.1

Query Match 58.9%; Score 53; DB 2; Length 184;
Best Local Similarity 90.0%; Pred. No. 9.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPYLPRLPRPP 12
|||:|:|:|
DB 26 RPPYLPRLPRPP 35

RESULT 14

S35332

apidaecin 73 precursor - honeybee (fragment)

N;Contains: apidaecin 1a

C;Species: Apis mellifera (honeybee)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Nov-2000

A;Accession: S35332; S05383

R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.

EMBO J. 12, 1569-1578, 1993

A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplifi

A;Reference number: S35330; MUID:93223697; PMID:8467807

A;Accession: S35332

A;Molecule type: mRNA

A;Residues: 1-283 <CAS>

A;Cross-references: EMBL:X72577; NID:g297066; PIDN:CAA51169.1; PID:g4539289

A;Accession: S05383

A;Molecule type: protein

A;Residues: 258-283 <CA3>

C;Superfamily: proline-rich protein

F;266-283/Product: apidaecin 1a #status experimental <MAT>

Query Match 58.9%; Score 53; DB 2; Length 283;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15
|||:|:|:|
DB 45 RPVIQPRPP 55

RESULT 15

E71415

probable coll wall protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: Columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C;Accession: E71415

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D.

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzensagger, T.; Pohl, T.M.; Terry, N.; G.

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;

C.; Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tl

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: E71415

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-428 <REV>
 A;Cross-references: GB:297338; NID:g2244870; PID:e327461; PID:g2244874
 C;Genetics:
 A;Map position: 4COP9-4G3845

Query Match 58.9%; Score 53; DB 2; Length 428;
 Best Local Similarity 61.5%; Pred. NO. 21;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRPYPYLPYRPP 15
 : |||||: ||||
 Db 67 KPPYPYIPCPYPP 79

Search completed: October 1, 2003, 19:06:09
 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 18:53:22 ; Search time 22 Seconds
(without alignments)

32.064 Million cell updates/sec

Title: US-09-426-011D-3

Perfect score: 90

Sequence: 1 RRRPRPPYLPRPPP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	90	100.0	172	1 PR39_PIG	P80054 sus scrofa
2	66	73.3	190	1 BCT7_BOVIN	P19661 bos taurus
3	59.5	66.1	107	1 COTT_BACSU	P11863 bacillus su
4	58	64.4	190	1 BCT7_SHEEP	P50415 ovis aries
5	56.5	62.8	168	1 AP14_APIME	Q06601 apis mellif
6	55.5	61.7	151	1 RNB_HSV2H	P89479 herpes simp
7	54	60.0	955	1 T150_HUMAN	Q9V241 homo sapien
8	53	58.9	144	1 AP22_APIME	P35581 apis mellif
9	53	58.9	283	1 AP73_BOVIN	Q9GK88 bos taurus
10	53	58.9	361	1 RL1_HSV2H	P28283 herpes simp
11	52	57.8	261	1 RL1_HSV2H	Q92858 homo sapien
12	52	57.8	354	1 AFCH_ARATH	P51566 arabidopsis
13	52	57.8	467	1 AFCH_ARATH	P51566 arabidopsis
14	52	57.8	841	1 REL4_STEAT	O85709 streptomyce
15	51.5	57.2	1187	1 PTNE_HUMAN	Q15678 homo sapien
16	51.5	57.2	1189	1 PTNE_MOUSE	Q62130 mus musculus
17	51	56.7	15	1 MK1_PALPR	P80408 palomona pr
18	51	56.7	180	1 XG_HUMAN	P55808 homo sapien
19	50.5	56.1	393	1 CIW4_HUMAN	Q9NV88 homo sapien
20	50.5	56.1	1095	1 AT17_HUMAN	O8t556 homo sapien
21	50	55.6	17	1 ACRO_BOMPA	P81464 bombus pasc
22	50	55.6	415	1 ACRO_PIG	P08001 sus scrofa
23	50	55.6	424	1 S3B4_HUMAN	Q15427 homo sapien
24	50	55.6	449	1 ABPP_BRANA	P40803 brassica na
25	50	55.6	678	1 ABPP_RIPCL	Q27305 riptortus c
26	49	54.4	134	1 PRL5_HUMAN	Q99354 homo sapien
27	49	54.4	296	1 GDA6_WHEAT	P04726 triticum ae
28	49	54.4	352	1 RRS1_ARATH	Q98488 arabidopsis
29	49	54.4	2911	1 FBZ2_HUMAN	P35556 homo sapien
30	48.5	53.9	2142	1 BAT2_HUMAN	P48334 homo sapien
31	48	53.3	280	1 TNF6_CERTO	Q9bnd1 cercocebus
32	48	53.3	280	1 TNF6_MACMU	Q9myl6 macaca mula
33	48	53.3	281	1 TNF6_HUMAN	P48023 homo sapien

ALIGNMENTS

RESULT 1

PR39_PIG

ID PR39_PIG STANDARD; PRT; 172 AA.

AC P80054; QSTR84; DT 01-MAR-1992 (Rel. 21, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Antibacterial protein PR-39 precursor.

GN PR39

OS Sus scrofa (Pig)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=95350216; PubMed=7624374;

RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,

RA Andersson L., Boman H.G.;

RT "Structure of the gene for porcine peptide antibiotic PR-39, a

RT cathelin gene family member: comparative mapping of the locus for the

RT human peptide antibiotic PAL-39.,"

RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).

RN (2)

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=94071853; PubMed=8250863;

RA Storici P., Zanetti M.;

RT "A cDNA derived from pig bone marrow cells predicts a sequence

RT identical to the intestinal antibacterial peptide PR-39.,"

RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).

RN (3)

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96105365; PubMed=7498526;

RA Zhao C., Ganz T., Lehrer R.I.;

RT "Structures of genes for two cathelin-associated antimicrobial

RT peptides: prophenin-2 and PR-39.,"

RL FEBS Lett. 376:130-134(1995).

RN (4)

RP SEQUENCE OF 131-169.

RC TISSUE=Intestine;

RX MEDLINE=92111534; PubMed=1765098;

RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,

RA Mutt V., Joernvall H.;

RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new

RT member of the family of proline-arginine-rich antibacterial

RT peptides.,"

RL Eur. J. Biochem. 202:849-854(1991).

RN (5)

RP SEQUENCE OF 131-164, AND FUNCTION.

RC TISSUE=Neutrophils;

RX MEDLINE=95088504; PubMed=7996056;

RA Shi J., Ross C.R., Chengappa M.M., Blecha P.;

RT "Identification of a proline-arginine-rich antibacterial peptide from

RT neutrophils that is analogous to PR-39, an antibacterial peptide from

RT the small intestine.,"

RN (6)

J. Leukoc. Biol. 56:807-811(1994).
CC -1- FUNCTION: EXERTS A POTENT ANTIMICROBIAL ACTIVITY AGAINST BOTH
CC E. COLI AND B. MEGATERIUM.
CC -1- TISSUE SPECIFICITY: SMALL INTESTINE AND BONE MARROW.
CC -1- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.

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CC EMBL; X87236; CAA60682.1; -
CC EMBL; L23825; AAA31109.1; -
CC EMBL; X89201; CAA61487.1; -
CC PIR; S68232; S69232.
CC InterPro: IPR001894; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC ProSITE; PS00946; CATHHELICIDINS 1; 1.
CC ProSITE; PS00947; CATHHELICIDINS 2; 1.
CC Antibiotic; Amigation; Signal; Pyrrolidone carboxylic acid.
CC SIGNAL 1 29
CC PROPEP 30 130
CC MOD_RES 30 30
CC DISULFID 85 96
CC DISULFID 107 124
CC MOD_RES 159 169
CC CONFLICT 21 21
CC CONFLICT 29 29
CC CONFLICT 90 91
CC CONFLICT 117 119
CC CONFLICT 157 157
CC SEQUENCE 172 AA; 19476 MW; 994B792798C0E133 CRC64;

Query Match 100.0%; Score 90; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 15
DB 131 RRRPRPPYLP RPRP 145

RESULT 2
BCT7 BOVIN STANDARD; PRG; 190 AA.
AC P1966L;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bactenecin 7 precursor (BAC7) (PR-59).
GN BAC7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95010707; PubMed=7925973;
RA Scocchi M., Romeo D., Zanetti M.;
RT "Molecular cloning of Bact7, a proline- and arginine-rich
RL antimicrobial peptide from bovine neutrophils.";
RN FBS Lett. 352:197-200 (1994).
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;

RA Scocchi M., Wang S., Zanetti M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 131-189.
RC TISSUE=Neutrophils;
RX MEDLINE=91035404; PubMed=2229048;
RT "Amino acid sequences of two proline-rich bactericins. Antimicrobial
RT peptides of bovine neutrophils.";
RL J. Biol. Chem. 265:18871-18874 (1990).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96300243; PubMed=8706679;
RA Storici P., Tossi A., Lenarcic B., Romeo D.;
RT "Purification and structural characterization of bovine
RT cathelicidins, precursors of antimicrobial peptides.";
RL Eur. J. Biochem. 238:769-776 (1996).
CC -1- FUNCTION: EXERTS IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC OF SUSCEPTIBLE MICROORGANISMS.
CC -1- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.
CC -1- PTM: ELASTASE IS RESPONSIBLE FOR ITS MATURATION.
CC -1- MASS SPECTROMETRY: MW=18395; MW_ERR=1; METHOD=Electrospray;
CC RANGE=30-190.
CC -1- SIMILARITY: BELONGS TO THE CATHHELICIDIN FAMILY.

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CC EMBL; L42977; AAA87359.1; -
CC EMBL; Y09471; CAA70616.1; -
CC InterPro: IPR001894; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC ProSITE; PS00946; CATHHELICIDINS 1; 1.
CC ProSITE; PS00947; CATHHELICIDINS 2; 1.
CC Antibiotic; Repeat; Signal; Pyrrolidone carboxylic acid.
CC SIGNAL 1 29
CC PROPEP 30 130
CC CHAIN 131 190
CC PROPEP 189 190
CC MOD_RES 30 30
CC DISULFID 85 96
CC DISULFID 107 124
CC SEQUENCE 190 AA; 21567 MW; 8CD07D7AA30A731C CRC64;

Query Match 73.3%; Score 66; DB 1; Length 190;
Best Local Similarity 85.7%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRPRPPYLP RPRP 14
DB 132 RRRPRPPYLP RPRP 145

RESULT 3
COTT_BACSU STANDARD; PRG; 107 AA.
ID COTT_BACSU
AC F11863;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Spore coat protein T precursor.
GN COTT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=168 / JH642;
RX  MEDLINE=89313296; PubMed=2546006;
RA  Aronson A.I., Song H.Y., Bourne N.;
RT  "Gene structure and precursor processing of a novel Bacillus subtilis
RL  spore coat protein.";
RL  Mol. Microbiol. 3:437-444(1989).
(2)
RN  SEQUENCE FROM N.A.
RP  STRAIN=168;
RX  MEDLINE=98044033; PubMed=9384377;
RA  Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA  Azevedo V., Bertero M.G., Bessières P., Bolotin A., Borchert S.,
RA  Borriess R., Boursier L., Brans A., Braun M., Brignelli S.C., Bron S.,
RA  Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA  Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA  Denizot F., Devine K.M., Dusterhoft A., Errlich S.D., Emerson P.T.,
RA  Entlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA  Friez C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA  Ghim S.Y., Glaser P., Goffeau A., Gollighly E.J., Grandi G.,
RA  Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA  Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA  Joris B., Karimata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA  Kobayashi Y., Koeter P., Konigstein G., Krogh S., Kumano M.,
RA  Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA  Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA  Meudone N., Mellado R.P., Mizuno M., Moesli D., Nakai S., Noback M.,
RA  Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA  Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA  Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA  Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA  Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA  Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Solido B.,
RA  Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA  Takeuchi M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA  Tossato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretti A.,
RA  Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA  Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA  Yoshida K., Yoshikawa H.F., Zumein E., Zumein E., Yoshikawa H., Danchin A.;
RT  "The complete genome sequence of the Gram-positive bacterium Bacillus
RT  subtilis.";
RL  Nature 390:249-256(1997).
CC  -!- FUNCTION: POSSIBLY PROTECTION OF SPORE AND PROBABLY PLAYS
CC  SOME ROLE IN GERMINATION.
CC  -!- SUBCELLULAR LOCATION: OUTER SURFACE OF ENDOSPORE.
CC
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC  or send an email to license@isb-sib.ch).
CC
CC  EMBL; X13740; CAAJ2004.1; -
CC  EMBL; Z59110; CABJ3066.1; -
CC  PIR; S04835; A41051.
CC  Subtilisin; BG10495; cotT.
CC  Sporulation; Signal; Complete proteome.
CC  SIGNAL 1 44
CC  CHAIN 45 107 SPORE COAT PROTEIN T.
CC  SEQUENCE 107 AA; 12992 MW; AD1F6F0C4CE29A3 CRC64;
CC
CC  Query Match 66.1%; Score 59.5; DB 1; Length 107;
CC  Best Local Similarity 84.6%; Pred. No. 0.6;
CC  Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
CC
CC  QY 4 PRPP-YLPRPRPP 15
CC  |||||
CC  DB 74 PREPPYPRPRPP 86

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RESULT 4
BCT7 SHEEP STANDARD; PRT; 190 AA.
ID BCT7 SHEEP STANDARD; PRT; 190 AA.
AC P50415;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bactescin 7 precursor (BAC7).
GN BAC7.5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_taxonomy:9940;
OX [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow; PubMed=7498547;
RA Bagella L., Scocchi M., Zanetti M.;
RA MEDLINE=96105386; PubMed=7498547;
RA "cDNA sequences of three sheep myeloid cathelicidins.";
RL FEBS Lett. 376:225-228(1995).
CC -!- FUNCTION: EXERTS, IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC OF SUSCEPTIBLE MICROORGANISMS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L46852; AAA85468.1; -
CC PIR; S68230; S68230.
CC InterPro; IPR001894; Cathelicidin.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHELICIDINS_2; 1.
CC KW Antibiotic; Repeat; Signal; Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC PROPEP 30 130 BY SIMILARITY.
CC CHAIN 131 190 BACTENECIN 7.
CC FT MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID
CC (BY SIMILARITY).
CC FT DISULFID 85 96 BY SIMILARITY.
CC FT DISULFID 107 124 BY SIMILARITY.
CC SQ SEQUENCE 190 AA; 21829 MW; E4AAFBI600E98371 CRC64;
CC
CC Query Match 64.4%; Score 59; DB 1; Length 190;
CC Best Local Similarity 78.6%; Pred. No. 1.6;
CC Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 RRRPRPPYLPRLPRP 14
CC |||||
CC DB 132 RLPRPRPLPRPRP 145

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RESULT 5
AP14 APINE STANDARD; PRT; 168 AA.
ID AP14 APINE STANDARD; PRT; 168 AA.
AC Q06601; P11525; P11526; P11527;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apidacin precursor, type 14.
GN APID14.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Megopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

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CC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93223697; PubMed=8467807;
RA Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT "Apidaecin multipetide precursor structure: a putative mechanism for
RT amplification of the insect antibacterial response.";
RL EMBO J. 12:1589-1578 (1993).
RN [2]
RP SEQUENCE OF APIDAEACIN IA/IB/II.
RC TISSUE=Hemolymph;
RX MEDLINE=90005446; PubMed=2676519;
RA Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT "Apidaecins: antibacterial peptides from honeybees.";
RL EMBO J. 8:2387-2391 (1989).
CC -!- FUNCTION: APIDAEACIN HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC PROPAGATION.
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CC -----
DR EMBL; X72575; CAB51167.1; -
DR PIR; S35330; S35330.
DR InterPro; IPR004828; Apidaecin.
DR Pfam; PF00807; Apidaecin; 5.
KW Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19
FT PROPEP 20 42
FT PEPTIDE 43 60
FT PROPEP 63 70
FT PEPTIDE 71 88
FT PROPEP 91 98
FT PEPTIDE 99 116
FT PROPEP 119 124
FT PEPTIDE 125 142
FT PROPEP 145 150
FT PEPTIDE 151 168
FT PEPTIDE 168 AA; 19380 MW; 594B931254C04A37 CRC64;
SQ SEQUENCE 168 AA; 19380 MW; 594B931254C04A37 CRC64;

Query Match 62.8%; Score 56.5; DB 1; Length 168;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

OY 1 RRRP-----RPPVLPVPRPP 15
DB 117 RREPEAEPGNRPVQIPRPP 138

RESULT 6
RNB_HSV2H
ID RNB_HSV2H STANDARD; PRT; 151 AA.
AC P89479;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Potential RNA-binding protein.
GN US11.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10315;
RN [1]
RP SEQUENCE FROM N.A.
RA Dolan A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: BINDS DNA AND RNA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z86099; CAB06719.1; -
DR DNA-binding; RNA-binding; Repeat; Nuclear protein.
FT DOMAIN 90 146
FT REPEAT 90 95
FT REPEAT 96 101
FT REPEAT 102 104
FT REPEAT 105 110
FT REPEAT 111 116
FT REPEAT 117 122
FT REPEAT 123 128
FT REPEAT 129 130
FT REPEAT 131 134
FT REPEAT 135 140
FT REPEAT 141 146
FT REPEAT 146 151
SQ SEQUENCE 151 AA; 16297 MW; FAB751F23C3DB6AE CRC64;

Query Match 61.7%; Score 55.5; DB 1; Length 151;
Best Local Similarity 73.3%; Pred. No. 2.4;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 RRRPPVLPVPRPP 15
DB 127 RPPPPVPRPPVPRPP 141

RESULT 7
T150 HUMAN
ID T150 HUMAN STANDARD; PRT; 955 AA.
AC Q9Y2W1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Thyroid hormone receptor-associated protein complex 150 kDa component
DE (Trap150).
GN TRAP150.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92214851; PubMed=10198638;
RA Ito M., Yuan C.-X., Malik S., Gu W., Pondell J.D., Yamamura S.,
RA Fu Z.-Y., Zhang X., Qin J., Roeder R.G.;
RT "Identity between TRAP and SMCC complexes indicates novel pathways for
RT the function of nuclear receptors and diverse mammalian activators.";
RL Mol. Cell 3:361-370 (1999).
RN [2]
RP SEQUENCE OF 1-672 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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DR EMBL; X72577; CAA51169.1; --

DR PIR; S06675; S06675.

DR PIR; S35332; S35332.

DR InterPro; IPR004828; Apidaecin.

DR Pfam; PF00807; Apidaecin; 9.

KW Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family; Cleavage on pair of basic residues; Repeat.

FT NON TER 1 1

FT SIGNAL <1 18 POTENTIAL.

FT PROPEP 19 41

FT PEPTIDE 42 59 APIDAEACIN IB.

FT PROPEP 62 69

FT PEPTIDE 70 87 APIDAEACIN IB.

FT PROPEP 90 97

FT PEPTIDE 98 115 APIDAEACIN.

FT PROPEP 118 125

FT PEPTIDE 126 143 APIDAEACIN IB.

FT PROPEP 146 153

FT PEPTIDE 154 171 APIDAEACIN.

FT PROPEP 174 182

FT PEPTIDE 183 199 APIDAEACIN IB.

FT PROPEP 202 209

FT PEPTIDE 210 227 APIDAEACIN IB.

FT PROPEP 230 237

FT PEPTIDE 238 255 APIDAEACIN IB.

FT PROPEP 258 265

FT PEPTIDE 266 283 APIDAEACIN IA.

SQ SEQUENCE 283 AA; 4EA5FEDECDS142B CRC64;

Query Match 58.9%; Score 53; DB 1; Length 283;

Best Local Similarity 72.7%; Pred. No. 8.7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 RPPYLPRLPRPP 15

DB 45 REVYIPQPRPP 55

RESULT 10

PRLP_BOVIN STANDARD; PRT; 381 AA.

AC Q9GKN8;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Prolargin precursor (Proline-arginine-rich end leucine-rich repeat protein).

GN PRELP.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

OX [1]

RN [1]

RP TISSUE=Articular cartilage;

RC MEDLINE=20576219; PubMed=11007795;

RA Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.; "The amino-terminal part of PRELP binds to heparin and heparan sulfate";

RT J. Biol. Chem. 275:40695-40702(2000).

RL [2]

RN [2]

RP FUNCTION.

RA MEDLINE=21964083; PubMed=11847210;

RA Bengtsson E., Moergelin M., Sasaki T., Timpi R., Heinegaard D., Aspberg A.; "The leucine-rich repeat protein PRELP binds perlecan and collagens and may function as a basement membrane anchor";

RT J. Biol. Chem. 277:15061-15068(2002).

RL

CC -!- FUNCTION: May anchor basement membranes to the underlying connective tissue.

CC -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan perlecan and triple helical collagens type I and type II.

CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

CC -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and heparan sulfate. Binds collagens type I and type II through its leucine-rich repeat domain.

CC -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS II SUBFAMILY.

CC -!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC -----

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CC -----

CC EMBL; AF163568; AAC23723.1; --

CC InterPro; IPR001611; LRR.

CC InterPro; IPR000372; LRR Nterm.

CC InterPro; IPR003591; LRR_Typ.

CC Pfam; PF00560; LRR; 9.

CC Pfam; PF01462; LRRNT; 1.

CC PRINTS; PR00019; LEURICHREP.

CC SMART; SM00013; LRRNT; 1.

KW Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat; Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 381 PROLARGIN.

FT DOMAIN 72 88 CIS-RICH.

FT REPEAT 94 113 LRR-S 1.

FT REPEAT 114 137 LRR-T 1.

FT REPEAT 138 161 LRR-T 2.

FT REPEAT 162 182 LRR-S 2.

FT REPEAT 183 206 LRR-T 3.

FT REPEAT 207 232 LRR-T 4.

FT REPEAT 233 253 LRR-S 3.

FT REPEAT 254 277 LRR-T 5.

FT REPEAT 278 302 LRR-T 6.

FT REPEAT 303 322 LRR-S 4.

FT REPEAT 323 361 LRR-T 7.

FT REPEAT 362 381 LRR-T 8.

FT DOMAIN 196 201 POLY-LEU.

FT DISULFID 331 372 BY SIMILARITY.

FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 381 AA; 43682 MW; 23DA99C01BB772A0 CRC64;

Query Match 58.9%; Score 53; DB 1; Length 381;

Best Local Similarity 76.9%; Pred. No. 12;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRPRLPRPP 14

DB 25 RRPRLPRPP 37

RESULT 11

RL1_HSV2H STANDARD; PRT; 261 AA.

ID RL1_HSV2H

AC P26233;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Neurovirulence factor (ICP34.5).

GN RL1.

OS Herpes simplex virus (type 2 / strain HG52).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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CC Alphaherpesvirinae; Simplexvirus.
CC NCBI_TaxID=10315;
CC [1]
CC MEDLINE=92113549; PubMed=1662697;
CC McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
CC "Comparative sequence analysis of the long repeat regions and
CC RT adjoining parts of the long unique regions in the genomes of herpes
CC RT simplex viruses types 1 and 2."
CC J. Gen. Virol. 72:3057-3075(1991).
CC [2]
CC SEQUENCE FROM N.A.
CC Dolan A.;
CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; D10471; BAA23428.1; -
CC EMBL; 286099; CAB06759.1; -
CC EMBL; 286099; CAB06706.1; -
CC PIR; JQ1502; WBEEXE.
CC Repeat.
CC FT DOMAIN 3 12 2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
CC FT REPEAT 3 7
CC FT REPEAT 8 12
CC FT DOMAIN 16 31 2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
CC FT REPEAT 16 23 V.
CC FT REPEAT 24 31
CC FT SEQUENCE 261 AA; 27908 MW; 4BBD13AF3D906D71 CRC64;
CC
CC Query Match 57.8%; Score 52; DB 1; Length 261;
CC Best Local Similarity 64.7%; Pred. No. 10;
CC Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
CC
CC QY 1 RRRPRP--FYLPRPRPP 15
CC DB 13 RRRPRPGAPVPRPGAP 29
CC
CC RESULT 12
CC ATH1_HUMAN STANDARD; PRT; 354 AA.
CC AC Q92858;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE Atonal protein homolog 1 (Helix-loop-helix protein HATH-1).
CC GN ATOH1 OR ATH1.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=97026280; PubMed=8872459;
CC Ben-Arie N., McCall A.B., Berkman S., Eichele G., Bellen H.J.,
CC Zoghbi H.Y.;
CC "Evolutionary conservation of sequence and expression of the bHLH
CC protein Atonal suggests a conserved role in neurogenesis.";
CC Hum. Mol. Genet. 5:1207-1216(1996).
CC CC -1- FUNCTION: ACTIVATES E BOX-DEPENDENT TRANSCRIPTION IN COLLABORATION
CC WITH E47, BUT THE ACTIVITY IS COMPLETELY ANTAGONIZED BY THE
CC NEGATIVE REGULATOR OF NEUROGENESIS HES-1. MAY PLAY A ROLE IN THE
CC DIFFERENTIATION OF SUBSETS OF NEURAL CELLS BY ACTIVATING E BOX-
CC DEPENDENT TRANSCRIPTION (BY SIMILARITY).
CC CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another

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CC BHLH protein.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC
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CC
CC EMBL; U61148; AAB41305.1; -
CC TRANSFAC; T04544; -
CC Genew; HGNC:797; ATOH1.
CC MIM; 601461; -
CC GO; GO:0003700; P:transcription factor activity; TAS.
CC GO; GO:0007417; P:central nervous system development; TAS.
CC GO; GO:006366; P:transcription from Pol II promoter; TAS.
CC InterPro; IPR001092; HLH_basic.
CC Pfam; PF00010; HLH; 1.
CC SMART; SM00353; HLH; 1.
CC PROSITE; PS00038; HLH 1; FALSE_NEG.
CC PROSITE; PS00888; HLH 2; 1.
CC KW Transcription regulation; Activator; DNA-binding; Nuclear protein.
CC FT DOMAIN 29 38 POLY-PRO.
CC FT DNA_BIND 160 171 BASIC DOMAIN
CC FT DOMAIN 172 212 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
CC FT DOMAIN 224 228 POLY-PRO.
CC FT SEQUENCE 354 AA; 38160 MW; AB12F1E917A00A8D CRC64;
CC
CC Query Match 57.8%; Score 52; DB 1; Length 354;
CC Best Local Similarity 57.1%; Pred. No. 14;
CC Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 2 RRRPRP--FYLPRPRPP 15
CC DB 21 RRRPRP--FYLPRPRPP 34
CC
CC RESULT 13
CC AFCL_ARATH STANDARD; PRT; 467 AA.
CC AC P51566; Q39184;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Protein kinase AFCL (EC 2.7.1.-).
CC GN AFCL OR AME2 OR AY3G53570 OR F4P12_270.
CC OS Arabidopsis thaliana (Mouse-ear cress).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
CC OX NCBI_TaxID=3702;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. landsberg erecta;
CC MEDLINE=95083650; PubMed=7991592;
CC Bender J., Fink G.R.;
CC "AFCL, a LAMMER kinase from Arabidopsis thaliana, activates STE12-
CC dependent processes in yeast.";
CC Proc. Natl. Acad. Sci. U.S.A. 91:12105-12109(1994).
CC [2]
CC SEQUENCE FROM N.A.
CC Kurokawa T., Yamamoto M.;
CC "A.thaliana genes encoding protein kinases of a new family.";
CC Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Columbia;
CC MEDLINE=21016720; PubMed=11130713;
CC Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

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RA Farntann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Botry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Cholsne N., Alliguenave F., Robert C., Brotier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erle H., Jordán R., Brandt S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brangert P.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loebner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Tazol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Laude M., Berger-Llauro C., Purnelle B., Masny D.,
RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A.C., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.V., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.B., White O., Venter J.C.,
RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Tabata S.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana".
RL Nature 408:820-822(2000).
CC -!- FUNCTION: ACTIVATOR OF YEAST TRANSCRIPTION FACTOR, STE12.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC LAMMER SUBFAMILY.
CC
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CC
CC EMBL: U16176; AAA57117.1; -
CC DR EMBL: D45354; BAA08215.1; -
CC DR EMBL: AL132966; CAB67664.1; -
CC DR PIR: S71169; S71169.
CC DR HSP: P24941; IAQ1.
CC DR InterPro: IPR007119; Prot kinase.
CC DR InterPro: IPR002230; Ser thr kinase.
CC DR InterPro: IPR001245; Tyr kinase.
CC DR Pfam: PF00069; pkinase; 1.
CC DR ProDom: PD000001; Prot kinase; 1.
CC DR SMART: SK00220; S_TKc; 1.
CC DR SMART: SK00219; TYKc; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC KW Transferase: Serine/threonine-protein kinase; ATP-binding.
CC FT DOMAIN 115 443 PROTEIN KINASE.
CC FT NP BIND 121 129 ATP (BY SIMILARITY).
CC FT BINDING 144 144 ATP (BY SIMILARITY).
CC FT ACT SITE 240 240 BY SIMILARITY.
CC FT CONFLICT 117 117 I -> M (IN REF. 1).
CC SQ SEQUENCE 467 AA; 54198 MW; A885FD32CE1B181 CRC64;

Query Match 57.8%; Score 52; DB 1; Length 467;
Best Local Similarity 52.4%; Pred. No. 18;
Matches 11; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 1 RRRPR-----PPYPRPRPP 15
DB 35 RRRPRUTWDAPPLPPPPPP 55

RESULT 14
DB 35 RRRPRUTWDAPPLPPPPPP 55
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).

RELAT STRAT STANDARD; PRT; 841 AA.
ID 085709;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE GTP pyrophosphokinase (EC 2.7.6.5) (ATP:GTP 3'-pyrophosphotransferase)
DE (ppGpp synthetase I) ((P)ppGpp synthetase).
DE RELA
GN Streptomyces antibioticus.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID:1890;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:IMRU 3720;
RX MEDLINE:99296594; PubMed:10368159;
RA Hoyt S., Jones G.H.;
RT "relA is required for actinomycin production in Streptomyces
RT antibioticus".
RL J. Bacteriol. 181:3824-3829(1999).
CC -!- FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5'-
CC diphosphate) is a mediator of the stringent response that
CC coordinates a variety of cellular activities in response to
CC changes in nutritional abundance. This enzyme catalyzes the
CC formation of ppGpp which is then hydrolyzed to form ppGpp (By
CC similarity) is required for actinomycin production.
CC -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
CC triphosphate.
CC -!- PATHWAY: ppGpp metabolism; first step.
CC -!- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF072829; AAC36021.1; -
CC DR InterPro: IPR002912; ACT.
CC DR InterPro: IPR006674; HD.
CC DR InterPro: IPR003607; Met phosphohydro.
CC DR InterPro: IPR004811; Spot_rela.
CC DR InterPro: IPR004095; TGS_dom.
CC DR Pfam: PF01842; ACT; 1.
CC DR Pfam: PF01966; HD; 1.
CC DR Pfam: PF04607; RelA_Spot; 1.
CC DR Pfam: PF02824; TGS; 1.
CC DR SMART: SM00471; HDC; 1.
CC DR TIGRFAMs: TIGR00691; spot_rela; 1.
CC KW Antibiotic biosynthesis; Transferase; Kinase.
CC SQ SEQUENCE 841 AA; 93671 MW; 632A037BA4EF4C94 CRC64;

Query Match 57.8%; Score 52; DB 1; Length 841;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRPPPPVLP RP RP 15
DB 50 RPKAPPRPPPP 64

RESULT 15
PTNE HUMAN
ID PTNE HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).

RELAT STRAT STANDARD; PRT; 841 AA.
ID 085709;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE GTP pyrophosphokinase (EC 2.7.6.5) (ATP:GTP 3'-pyrophosphotransferase)
DE (ppGpp synthetase I) ((P)ppGpp synthetase).
DE RELA
GN Streptomyces antibioticus.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID:1890;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:IMRU 3720;
RX MEDLINE:99296594; PubMed:10368159;
RA Hoyt S., Jones G.H.;
RT "relA is required for actinomycin production in Streptomyces
RT antibioticus".
RL J. Bacteriol. 181:3824-3829(1999).
CC -!- FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5'-
CC diphosphate) is a mediator of the stringent response that
CC coordinates a variety of cellular activities in response to
CC changes in nutritional abundance. This enzyme catalyzes the
CC formation of ppGpp which is then hydrolyzed to form ppGpp (By
CC similarity) is required for actinomycin production.
CC -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
CC triphosphate.
CC -!- PATHWAY: ppGpp metabolism; first step.
CC -!- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF072829; AAC36021.1; -
CC DR InterPro: IPR002912; ACT.
CC DR InterPro: IPR006674; HD.
CC DR InterPro: IPR003607; Met phosphohydro.
CC DR InterPro: IPR004811; Spot_rela.
CC DR InterPro: IPR004095; TGS_dom.
CC DR Pfam: PF01842; ACT; 1.
CC DR Pfam: PF01966; HD; 1.
CC DR Pfam: PF04607; RelA_Spot; 1.
CC DR Pfam: PF02824; TGS; 1.
CC DR SMART: SM00471; HDC; 1.
CC DR TIGRFAMs: TIGR00691; spot_rela; 1.
CC KW Antibiotic biosynthesis; Transferase; Kinase.
CC SQ SEQUENCE 841 AA; 93671 MW; 632A037BA4EF4C94 CRC64;

Query Match 57.8%; Score 52; DB 1; Length 841;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRPPPPVLP RP RP 15
DB 50 RPKAPPRPPPP 64
<

```

GN PTPN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains.";
RL Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -!- SIMILARITY: Contains 1 PFM domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC -----
CC EMBL; X82676; CAA57993.1; .
CC PIR; JC4155; JC4155.
CC HSP; P29350; IGWZ.
CC Genew; HGNC:9647; PTPN14.
CC MM; 603155.
CC GO; GO:0006470; P; protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR phosphatase.
CC InterPro; IPR000242; TYR_PP.
CC Pfam; PF00373; Band 4.1; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND4.1.
CC PRINTS; PR00700; PRTPHPTASE.
CC SMART; SM00295; B4.1; 1.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; PFM_1; 1.
CC PROSITE; PS00661; PFM_2; 1.
CC PROSITE; PS00587; PFM_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC KX Structural protein; Cytoskeleton; Hydrolase.
CC FT DOMAIN 21 306 FERM.
CC FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
CC FT ACT SITE 1121 1121 BY SIMILARITY.
CC FT DOMAIN 566 573 POLY-PRO.
CC FT DOMAIN 709 716 POLY-GLU.
CC SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;
Query Match 57.3%; Score 51.5; DB 1; Length 1187;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3 RPPPPYLRPRP 14
DB 565 RPPPPY-PRPRP 575

```

Search completed: October 1, 2003, 19:03:41
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 1, 2003, 19:00:08 ; Search time 93 seconds
(without alignments)
41.621 Million cell updates/sec

Title: US-09-426-011d-3

Perfect score: 90

Sequence: 1 RRRPPYLPFRPP 15

Scoring table: BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	67.8	336	12 Q68405	Q68405 human cytom
2	58	64.4	156	10 Q8RV32	Q8RV32 oryza sativ
3	58	64.4	184	6 P79361	P79361 ovis aries
4	58	64.4	190	6 Q9XSQ9	Q9XSQ9 capra hircu
5	58	64.4	224	6 O19031	O19031 ovis aries
6	58	64.4	1729	10 Q8LLZ0	Q8LLZ0 oryza sativ
7	57.5	63.9	183	10 Q94J98	Q94J98 oryza sativ
8	57	63.3	200	16 Q9RK54	Q9RK54 streptomyce
9	57	63.3	361	2 Q9XCG4	Q9XCG4 mycobacteri
10	56	62.2	212	2 O08306	O08306 nocardioide
11	55	61.1	212	12 Q41980	Q41980 murid herpe
12	55	61.1	464	12 Q91TM2	Q91TM2 tupiaia herp
13	54.5	60.6	301	10 Q41848	Q41848 zea mays (m
14	54.5	60.6	2635	12 Q40942	Q40942 kaposi's sa
15	54.5	60.6	2635	12 P89955	P89955 kaposi's sa
16	54	60.0	144	10 Q8LW3	Q8LW3 oryza sativ

ALIGNMENTS

RESULT 1

Q68405 ID Q68405 PRELIMINARY; PRT; 336 AA.

AC Q68405;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Orf UL151.

OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Toledo;

RX MEDLINE=96099416; PubMed=8523595;

RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;

RT "Human cytomegalovirus clinical isolates carry at least 19 genes not

found in laboratory strains.";

RL J. Virol. 70:78-83(1996).

DR EMBL; U33331; AAA85892.1; -

SQ SEQUENCE 336 AA; 35116 MW; 9F865B5019F69D0C CRC64;

Query Match 67.8%; Score 61; DB 12; Length 336;

Best Local Similarity 78.6%; Pred. No. 0.92;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRPPYLPFRPP 15

Db 279 RRRPPYLPFRPP 292

RESULT 2

Q8RV32 ID Q8RV32 PRELIMINARY; PRT; 156 AA.

AC Q8RV32;

DT 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

Q8RV32 mus musculu
Q9XZT0 drosophila
Q4582 caenorhabdi
Q95X63 caenorhabdi
Q8BV76 mus musculu
Q8BZ77 mus musculu
Q99JA6 mus musculu
Q8BKT2 mus musculu
Q9SM77 oryza sativ
Q23291 caenorhabdi
Q9JFF6 oryza sativ
Q8WE88 apis mellif
Q9XIZ3 oryza sativ
Q23370 arabidopsis
Q82066 solanum tub
Q9LV14 arabidopsis
Q66852 fowl adenov
Q8U5T2 agrobacteri
Q96E55 homo sapien
Q42421 beta vulgar
Q8T458 drosophila
Q8MME1 drosophila
Q9LMQ1 arabidopsis
Q9WZ6 drosophila
Q8V718 samian herp
Q8C3A1 oryza sativ
Q8CE88 mus musculu
Q8CAV9 mus musculu

DE OSJNB0032K15.1 protein (OJ1159 D09.32 protein).
 GN OSJNB0032K15.1 OR QJ1159 D09.32
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 RT clone:OSJNB0032K15.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 RT clone:OJ1159 D09.32";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003710; SAB86560.1; -;
 DR EMBL; AP003792; SAB89214.1; -;
 DR Gramene; O8RV22; -;
 SQ SEQUENCE 156 AA; 17659 MW; 4152112C3DB493CF CRC64;

Query Match 64.4%; Score 58; DB 10; Length 156;
 Best Local Similarity 73.3%; Pred. No. 1.1;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRPRRP 15
 |||||
 DB 78 RRRPRPPYLRPRRP 92

RESULT 3

P79361
 ID P79361 PRELIMINARY; PRT; 164 AA.
 AC P79361;
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE 7.5 kDa bactinecin (Fragment).
 GN BAC7.5.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;
 RT "Molecular analysis of the sheep cathelin family reveals a novel
 RT antimicrobial peptide.";
 RL FEBS Lett. 377:519-522(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Huttner K.M., Mahoney M.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U60598; A849713.1; -;
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 FT NON_TER 164 AA;
 SQ SEQUENCE 164 AA; 18642 MW; E3BF0871F6A8B9A CRC64;

Query Match 64.4%; Score 58; DB 6; Length 164;
 Best Local Similarity 78.6%; Pred. No. 1.2;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRRPRPPYLRPRRP 14
 |||||
 DB 132 RLRPRPRLPRRP 145

RESULT 4

Q9XSQ9
 ID Q9XSQ9 PRELIMINARY; PRT; 190 AA.
 AC Q9XSQ9;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE BAC7.5 protein.
 GN BAC7.5.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Zhao C., Nguyen T., Brogden K., Lehrer R.;
 RT "cDNA cloning of goat cathelin related peptides.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243125; CAB45523.1; -;
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 FT CHAIN 131 190 BAC7.5 PROTEIN.
 SQ SEQUENCE 190 AA; 21835 MW; D13305EF16875F4F CRC64;

Query Match 64.4%; Score 58; DB 6; Length 190;
 Best Local Similarity 78.6%; Pred. No. 1.3;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLRPRRP 14
 |||||
 DB 132 RLRPRPRLPRRP 145

RESULT 5

O19031
 ID O19031 PRELIMINARY; PRT; 224 AA.
 AC O19031;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE BACTINECIN 11 precursor.
 GN BAC11.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96140581; PubMed=8549789;
 RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
 RT "Localization and genomic organization of sheep antimicrobial peptides
 RT genes.";
 RL Gene 206:85-91(1998).
 CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
 DR EMBL; U77049; AAB62000.1; -;
 DR EMBL; U77047; AAB62000.1; JOINED.
 DR EMBL; U77048; AAB62000.1; JOINED.
 DR InterPro; IPR001894; Cathelicidin.

DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 KW Signal; Antibiotic.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 130 POTENTIAL.
 FT CHAIN 131 224 BACTINECIN 11.
 FT MOD_RES 30 30 PYROLIDONE CARBOXYLIC ACID (BY
 FT DISULFID 85 96 BY SIMILARITY).
 FT DISULFID 107 124 BY SIMILARITY.
 SQ SEQUENCE 224 AA; 25669 MW; 6AEAAAB1256AC76FC CRC64;

Query Match 64.4%; Score 58; DB 6; Length 224;
 Best Local Similarity 78.6%; Pred. No. 1.6;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 14
 |||||
 DB 132 RLPRPRPLPRP 145

RESULT 6
 ID Q8LLZ0 PRELIMINARY; PRT; 1729 AA.
 AC Q8LLZ0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative retroelement.
 GN OSJNAA0028C16.15.
 OS Oryza sativa (rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sasaki C.,
 RA Currie J., Collura K.;
 RT "Rice Genomic Sequence."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC131966; AAN04923.1; -.
 DR Gramene; Q8LLZ0; -.
 DR InterPro; IPR001969; Aspartate site.
 DR InterPro; IPR005162; Retrotrans_gag.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR000477; RYase.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF03732; Retrotrans_gag; 1.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00078; rvt; 2.
 DR Pfam; PF00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_CCHC; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS00158; ZF_CCHC; 1.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 1729 AA; 197883 MW; 6FA3642FD34B4E33 CRC64;

Query Match 64.4%; Score 58; DB 10; Length 1729;
 Best Local Similarity 73.3%; Pred. No. 11;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPRPPYLPRLPRP 15
 |||||
 DB 71 RRRPRPLRRRRPP 85

RESULT 7
 ID Q94J98 PRELIMINARY; PRT; 183 AA.

AC Q94J98;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE P0047B08.14 protein (OJ1159 D09.5 protein).
 GN P0047B08.14 OR OJ1159 D09.5.
 OS Oryza sativa (Rice), and
 Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530, 39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0047B08.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
 RT clone:OJ1159 D09.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003053; BAB55690.1; -.
 DR EMBL; AP003792; BAB89188.1; -.
 DR Gramene; Q94J98; -.
 SQ SEQUENCE 183 AA; 20155 MW; F1CF823AD89CEB36 CRC64;

Query Match 73.9%; Score 57.5; DB 10; Length 183;
 Best Local Similarity 73.3%; Pred. No. 1.5;
 Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRPRPPYLPRLPRP 15
 |||||
 DB 129 RSRPR-PYAPRPQP 142

RESULT 8

ID Q9RK54 PRELIMINARY; PRT; 200 AA.
 AC Q9RK54;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO0323.
 GN SCO0323 OR SCF12.02C
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953;
 RA Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Thomson N.R., James K.D., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Harper D., Bateman A., Brown S., Chandra G., Hornsby T., Howarth S.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Oliver K., O'Neill S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 DR EMBL; AL939105; CAB56128.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 200 AA; 22076 MW; 0DCBBEC5585803B5 CRC64;

QY 1 RRRPRPPYLPRLPRP 15
 |||||
 DB 129 RSRPR-PYAPRPQP 142

Query Match 53.3%; Score 57; DB 16; Length 200;
 Best Local Similarity 76.9%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 13
 |||||
 Db 118 RRRPPPPYLP RPR 130

RESULT 9
 Q9XCG4 PRELIMINARY; PRT; 361 AA.
 AC Q9XCG4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 40.2 kDa protein.
 OS Mycobacterium avium.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2151;
 RA Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
 RT "Identification of a gene cluster involved in glycopeptidolipid
 biosynthesis and of a gene cluster encoding daunorubicin resistance in
 two strains of Mycobacterium avium serovar 2";
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF143772; AAD44199.1;
 KW Hypothetical protein.
 SQ SEQUENCE 361 AA; 40208 MW; AD01DBB825C1C9EA CRC64;

Query Match 63.3%; Score 57; DB 2; Length 361;
 Best Local Similarity 71.4%; Pred. No. 3.4;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 14
 |||||
 Db 32 RRRPPPPYLP RPR 145

RESULT 10
 O08306 PRELIMINARY; PRT; 212 AA.
 ID O08306;
 AC O08306;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical 21.7 kDa protein.
 OS Nocardioideae simplex (Arthrobacter simplex).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Propionibacterineae; Nocardioidaceae; Pimelobacter.
 OX NCBI_TaxID=2045;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO12069;
 RA MEDLINE=95319331; PubMed=7536291;
 RA Molnar I., Choi K., Yamashita M., Murooka Y.;
 RT "Molecular cloning, expression in Streptomyces lividans, and analysis
 of a gene cluster from Arthrobacter simplex encoding 3-
 ketosteroid-DELTA.1-dehydrogenase, 3-ketosteroid-DELTA.5-isomerase
 and a hypothetical regulatory protein";
 RT Mol. Microbiol. 15:895-905 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO12069;
 RA Dziadek J., Yamashita M., Murooka Y.;
 RT "Cloning, sequencing and characterization of the downstream region of
 KsdDI operon of Arthrobacter simplex";
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
 REGULATORS.

DR EMBL; Z93338; CAB07542.1;
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr; 1.
 DR PRINTS; PR00455; HTH_TETR.
 DR PROSITE; PS01081; HTH_TETR_FAMILY; 1.
 KW Hypothetical protein; DNA-Binding; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 212 AA; 22740 MW; F9118E18DDF4E0B2 CRC64;

Query Match 62.2%; Score 56; DB 2; Length 212;
 Best Local Similarity 73.3%; Pred. No. 2.8;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRPPPPYLP RPR 15
 |||||
 Db 93 RRRPPPPYLP RPR 97

RESULT 11
 O41980 PRELIMINARY; PRT; 212 AA.
 ID O41980;
 AC O41980;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Hypothetical 21.9 kDa protein.
 GN GAMMAHV M13.
 OS Murid herpesvirus 4.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae.
 OX NCBI_TaxID=33708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WUMS;
 RX MEDLINE=97366649; PubMed=9223479;
 RA Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
 RA Dal Canto A.J., Speck S.H.;
 RT "Complete sequence and genomic analysis of murine gammaherpesvirus
 68";
 RT J. Virol. 71:5894-5904 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WUMS;
 RA Latreille P., Wamsley P., Waterston R.H.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97553; AAB6426.1;
 KW Hypothetical protein.
 SQ SEQUENCE 212 AA; 21911 MW; E066860064282149 CRC64;

Query Match 61.1%; Score 55; DB 12; Length 212;
 Best Local Similarity 75.0%; Pred. No. 3.8;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RRRPPPPYLP RPR 15
 |||||
 Db 136 RRRPPPPYLP RPR 147

RESULT 12
 Q91TM2 PRELIMINARY; PRT; 464 AA.
 ID Q91TM2;
 AC Q91TM2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE T74.
 OS Tupaia herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae.
 OX NCBI_TaxID=10397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2;

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RX MEDLINE=21211637; PubMed=11312357;
RA Bahr U., Darai G.;
RT "Analysis and Characterization of the Complete Genome of Tupaia (Tree
RL Shrew) Herpesvirus";
RL J. Virol. 75:4854-4870(2001).
RN SEQUENCE FROM N.A.
RC STRAIN=2;
RA Darai G., Bahr U.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201817; AAK57119.1; -.
SQ SEQUENCE 464 AA; 51193 MW; 4BB7313EA2C2ED16 CRC64;

Query Match 61.1%; Score 55; DB 12; Length 464;
Best Local Similarity 76.9%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRPYPYLPRPP 15
Db 421 RRPYPYPYPP 433

RESULT 13
Q41848 PRELIMINARY; PRT; 301 AA.
ID Q41848;
AC Q41848;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Prolin rich protein.
GN PRP.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
ON [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W64A;
RA MEDLINE=92361259; PubMed=1498600;
RA Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
RT "A maize embryo-specific gene encodes a proline-rich and hydrophobic
RT protein.";
RL Plant Cell 4:413-423(1992).
DR EMBL; X60432; CAA42959.1; -.
DR HSSP; P24337; LHYP.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF00234; trypt alpha amyl. 1.
DR PRINTS; PR01217; PRICHEXTENSN.
DR SMART; SM00499; AAI. 1
SQ SEQUENCE 301 AA; 31647 MW; 864EB70854D28C2E CRC64;

Query Match 60.6%; Score 54.5; DB 10; Length 301;
Best Local Similarity 71.4%; Pred. No. 6.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 RRPYPYLPRPP 15
Db 149 RSPYPYPP 162

RESULT 14
O40942 PRELIMINARY; PRT; 2635 AA.
ID O40942;
AC O40942;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ORF 64.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.

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OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RT "The genome of human herpesvirus 8 cloned from Kaposi's sarcoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93872; AAB62600.1; -.
DR InterPro; IPR006928; Herpes teg N.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF04843; Herpes teg N; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
SQ SEQUENCE 2635 AA; 289717 MW; 91DDA0D6FF7B660A CRC64;

Query Match 60.6%; Score 54.5; DB 12; Length 2635;
Best Local Similarity 68.4%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

Qy 2 RRPYPYPYPYPP 15
Db 271 RRPYPYPYPP 289

RESULT 15
P88955 PRELIMINARY; PRT; 2635 AA.
ID P88955;
AC P88955;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ORF 64.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
ON [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (SHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75698; AAC57149.1; -.
DR InterPro; IPR006928; Herpes teg N.
DR InterPro; IPR002965; P rich extensn.
DR Pfam; PF04843; Herpes teg N; 1.
DR PRINTS; PR01217; PRICHEXTENSN.
SQ SEQUENCE 2635 AA; 289667 MW; 00070132EA8139AF CRC64;

Query Match 60.6%; Score 54.5; DB 12; Length 2635;
Best Local Similarity 68.4%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 2;

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Qy 2 RRRP---PPVLP--RRPP 15
| | | | |
Db 271 RRPVVIPPYD&TDRPP 289

Search completed: October 1, 2003, 19:05:23
Job time : 95 secs